

Db 475 CPTSKKEEQGQEEQPPR----PTTEQLPPARPKSAELLQRYSPI----- 520
 Qy 52 TGLFGEEDVRFSSAPYM-----PTVYLRLTACAGCRSYTEAY----VTIPV 96
 Db 521 ----KKQVRFAASPMPQPERELCPQLPQSPSTLDGSQSSPTNAVSGPKKBLPPI 575
 Qy 97 GCTCVPEPEKDADSINNSIDKGAKLIGPNDA 130
 Db 576 ACR--PRPSNVSNSPNSS-----SPGSAP 597

RESULT 15

046545 ID 046545 PRELIMINARY; PRT; 1045 AA.
 AC 046545;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DR 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE COMPLEMENT RECEPTOR TYPE 2.
 GN CR2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_Taxid=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WHTHE ALPINE;
 RA Hein W. R., Dudley L., Marston W., Landsverk T., Young A., Avila D.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF038131; AAB92375.1;
 HSSP: P10988; IYVD;
 DR InterPro; IPR000436;
 DR Pfam; PF00084; sushi; 14.
 DR SMART; SM00032; CCP; 1.
 SQ SEQUENCE 1045 AA; 115561 MW; FF58E1A2892CD59 CRC64;

Query Match 10.6%; Score 77.5; DB 6; Length 1045;
 Best Local Similarity 25.9%; Pred. No. 8.7;
 Matches 29; Conservative 13; Mismatches 43; Indels 27; Gaps 5;
 Qy 15 PPTNLRSVSPMAIRISDPARYPRYLPEAYCLRCGLTG--LFGEDDVRFRSAPYMPYTV 72
 Db 423 PPKILNGQKEDHRVFDPGTSIRY-----SCDPGVLVGEBSIREPDGWLPITA 473
 Qy 73 VLRRTPACAGGRSVYTEAYTIPVGCTCYPEKD--ADSISSSIDKGAKL 122
 Db 474 PICKAAECE-----PVGRQVFKKPKNQFIRPDVNSSCD-EGYRL 511

Search completed: October 5, 2001, 15:23:45
 Job time: 190 sec

RP	SEQUENCE FROM N.A.	Db	455 SPWC-----STPRSPRSLSVCPDVAAFC-----SDMRWLRAPITIPMSLVR--	496	
RA	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases	Qy	79 ACAGG-----RSVYTEAYYTIP6CTCYPEPEKDADSINSSIDK	118	
RN	[2]	DB	497 -ADGLFYPSSAFSETYTPESYSVR-CHPVGPEPATDADLESIHQE	540	
RX	MEDLINE=94150718; PubMed=7906398;				
RA	Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,	RESULT	14		
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnstone L.,	Q9VFD4	PRELIMINARY;		
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones M., Kershaw J., Kirstein J., Laister N., Latreille P., Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R., Shihry-Mieg J., Thomas K., Vaughan K., Watson R., Watson A., Weinstock L., Wilkinson-Sprout J., Wohlgemuth R., elegans";	AC	PRT;	805 AA.	
RA	"2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";	DT	01-MAY-2000 (TREMBLrel. 13, Created)		
RA	Watson R., "2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
RA	Watson R., Staden R., Sulston J., RR	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
RA	CG18442 PROTEIN.	DE	CG18442. PROTEIN.		
RA	Drosophila melanogaster (Fruit fly).	GN	Drosophila melanogaster		
RA	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydioidea; Drosophilidae; Drosophila.	OS			
DR	NCBI_TaxID=227;	OC			
DR	NCBI_TaxID=11;	OX			
DR	InterPro: IPR001304; -.	RN	[11]		
DR	pfam; PF00059; lectin_C; 1.	RP	SEQUENCE FROM N.A.		
DR	SMART; SM00034; CLECT; 1.	RC	STRAIN=BERKELEY;		
SQ	SEQUENCE 226 AA; 24150 MW; DB4C40BFFF904200 CRC64;	RC	MEDLINE=20196006; PubMed=10731132;		
Query Match	Best Local Similarity 10.88, Score 78.5, DB 5, Length 226;	RA	Adams M.D., Celikiner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheerer S.E., Liu P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borrova D., Botchan M.R., Bouck P., Brodtier P., Burts K.C., Busam C.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K.V., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabriel A.E., Garg N.S., Gelbart W.M., Glasser K., Globek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston T.J., Wei K.A.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Lai P., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Leis Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein-D.R., Pacieb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puriv V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartskas R., Tector C., Turner R., Venter J., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Robin G.M., Venter J.C.;	RT	"The genome sequence of Drosophila melanogaster." NBL Science 287:2185-2195 (2000).
RA	InterPro: IPR002309; -.	RL	AE003707; AAF55126.1;		
DR	FBn0030287; CG18442.	DR	FlyBase; AE003707; AAF55126.1;		
SQ	SEQUENCE 552 AA; 60422 MW; SE2EC4B12237AF43 CRC64;	SQ	SEQUENCE 805 AA; 86321 MW; FDF9EFEFF14E69957 CRC64;	8;	
Query Match	Best Local Similarity 10.7%; Score 78; DB 4, Length 552;	RA	CPAGGR-----PRT;		
Matches	29.0%; Pred. No. 3.8;	RA	CPAGGR-----PRT;		
RA	SEQUENCE FROM N.A.	RA	CPAGGR-----PRT;		
RA	Bridgeman A.; Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	RA	CPAGGR-----PRT;		
RA	EMBL; AL021578; CAA16521.1; -.	RA	CPAGGR-----PRT;		
DR	InterPro: IPR002309; -.	RA	CPAGGR-----PRT;		
SQ	SEQUENCE 552 AA; 60422 MW; SE2EC4B12237AF43 CRC64;	RA	CPAGGR-----PRT;		
Query Match	Best Local Similarity 10.7%; Score 78; DB 5, Length 805;	RA	CPAGGR-----PRT;		
Matches	23.4%; Pred. No. 5.8;	RA	CPAGGR-----PRT;		
RA	SEQUENCE FROM N.A.	RA	CPAGGR-----PRT;		
RA	Bridgeman A.; Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.	RA	CPAGGR-----PRT;		
RA	EMBL; AL021578; CAA16521.1; -.	RA	CPAGGR-----PRT;		
DR	InterPro: IPR002309; -.	RA	CPAGGR-----PRT;		
SQ	SEQUENCE 552 AA; 60422 MW; SE2EC4B12237AF43 CRC64;	RA	CPAGGR-----PRT;		

RESULT	9	SEQUENCE	148 AA;	16738 MW;	ADB51F438DFB3940 CRC64;	
04 0633	PRELIMINARY;	PRT;	151 AA.			
ID 040633;						
AC 040633;						
DT 01-JAN-1998 (TREMBLrel. 05, Created)						
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)						
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)						
INTERLEUKIN 17.						
DE						
OS Saimiriine herpesvirus 2.						
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;						
OC Gammaherpesvirinae; Rhadinoviridae.						
NCBI_TAXID=10381;						
RN [1]						
SEQUENCE FROM N.A.						
STRAIN=C-888;						
RC						
RX MEDLINE=98037620; PubMed=9371569;						
RA Knappe A., Häßler C., Tharau M., Wittmann S., Hofmann H., Fleckenstein B., Flickenscher H.;						
RT The superantigen-homologous viral immediate-early gene iel4/vsg in herpesvirus saimiri transformed human T cells.;"						
RL J. Virol. 71:9124-9133 (1997).						
DR EMBL; Y13183; CAA73627.1; -.						
SQ SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;						
RESULT 11						
Q9UBG7	Query Match	13.6%;	Score 99;	DB 5;	Length 148;	
ID Q9UBG7	Best Local Similarity	29.8%;	Pred. No. 0.005;			
AC Q9UBG7;	Matches	35;	Indels	14;	Gaps 5;	
DT 01-MAY-2000 (TREMBLrel. 13, Created)	Conservative	17;	Mismatches			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)						
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
PAC -AGGSIVTEAYVTIPVGC-TCVPEEEKDA 108						
Db QY 78						
Db 104 -SCDRSTGLWNNYVRSTELITVGCHSVLPRTQRAA 136						
RESULT 12						
Q9XUH9	Query Match	10.9%;	Score 79.5;	DB 4;	Length 520;	
ID Q9XUH9	Best Local Similarity	28.3%;	Pred. No. 2.4;			
AC Q9XUH9;	Matches	12;	Mismatches	36;	Gaps 4;	
DT 01-NOV-1999 (TREMBLrel. 12, Created)	Conservative					
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)						
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
PRT; 226 AA.						
Caenorhabditis elegans.						
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;						
OC Rhabditidae; Peloderaeinae; Caenorhabditida.						
NCBI_TAXID=6239;						
RN [1]						
SEQUENCE FROM N.A.						
F25D1.3 PROTEIN.						
GN F25D1.3.						
RA Kelly P.						
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.						
RN [2]						
RESULT 13						
Q9XUH9	Query Match	10.9%;	Score 79.5;	DB 4;	Length 520;	
ID Q9XUH9	Best Local Similarity	28.3%;	Pred. No. 2.4;			
AC Q9XUH9;	Matches	12;	Mismatches	36;	Gaps 4;	
DT 01-NOV-1999 (TREMBLrel. 12, Created)	Conservative					
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)						
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
PRT; 226 AA.						
Caenorhabditis elegans.						
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;						
OC Rhabditidae; Peloderaeinae; Caenorhabditida.						
NCBI_TAXID=6239;						
RN [1]						
SEQUENCE FROM N.A.						
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Cossey T., Cooper J., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray J., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showken R., Smalldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaughn M., Waterston R., Watson A., Weinstock L., Wilkison Sprout J., Wohldman P., RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans." RT Nature 368:32-38 (1994). DR EMBL; Z733973; CAA98268.1; -.						
RL Nature 368:32-38 (1994). DR EMBL; Z733973; CAA98268.1; -.						

DE CYTOKINE-LIKE PROTEIN ZCYTO7 (NEURONAL INTERLEUKIN-17 RELATED FACTOR).
GN ZCYTO7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP Presnell S., Gilburt T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Presnell S., Gilburt T., Whitmore T.E., Gilburt T., Kuestner R.E.,
RA Smith D., Yao L., Whitmore T.E., Gilburt T., Kuestner R.E.,
RA Martinez T., Hoffman R., O'Hara P.;
RA Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RL
RN SEQUENCE FROM N.A.
RP Moore E.B., Presnell S., Garrigues U., Guillot A., LeGuenn E.,
RA Smith D., Yao L., Whitmore T.E., Gilburt T., Kuestner R.E.,
RT "Identification of a novel IL-17 related factor: Demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF184970; AAC013191; -.
DR EMBL: AF218726; AAC41351; -.
SQ SEQUENCE 180 AA; 20309 MW; E26F4C7201997C5 CRC64;

RESULT	6	PRT;	111 AA.
Q9EQT7		PRELIMINARY;	
ID	Q9EQ17		
AC	Q9EQ17;		
DT	01-MAR-2001 (TREMBL)	16, Created	
DT	01-MAR-2001 (TREMBL)	16, Last sequence update	
DT	01-MAR-2001 (TREMBL)	16, Last annotation update	
DE	NERF (FRAGMENT).		
OS	Rattus norvegicus (Rat).		
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.		

[1] R N SEQUENCE FROM N.A.
 RP Moore E. B., Presneil S., Garrigues U., Guilbot A., LeGuern E.,
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;
 RA "Identification of a novel II-17 related factor: Demonstration of
 RT neuronal expression and evaluation as a candidate for the chromosome
 RT 5g-linked form of Charcot-Marie-Tooth disease." ;
 RT Submitted (DEC-1998) ;
 RL EMBL; AF218724; AAC44133.1; - .
 DR 1
 NON_TER 1
 FT 111 111
 CO 111 111
 SC 111 111
 CR 111 111
 SR 111 111
 DR 111 111

Q9NUE6		PRELIMINARY;		PRT;	78 AA.
ID	Q9NUE6;				
AC	Q9NUE6;				
DT	01-OCT-2000	(TREMBrel.	15.	Created)	
DT	01-OCT-2000	(TREMBrel.	15.	Last sequence update)	
DT	01-OCT-2000	(TREMBrel.	15.	Last annotation update)	
DE	DJ108C2_3	(PUTATIVE NOVEL PROTEIN SIMILAR TO IL17 (INTERLEUKIN 1 CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED SERINE ESTERASE 8))		(CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED SERINE ESTERASE 8) (FRAGMENT).	
DE	DJ108C2_3.	Homo sapiens (Human).			
OS	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC					
OC	NCBI_TAXID=9606;				
OX	[1]				
SEQUENCE FROM N.A.					
RA	Almeida J.				
RL	Submitted (PEB-2000) to the EMBL/GenBank/DDBJ databases				
DR	EMBL: AL034343; CAB75300; 1;	-			
NON_TER	1	1			
FT					
SEQUENCE	78 AA:	8704 MW:	66C3C34E7ACC2790 CRC64;		
Query Match	16.4 %;	Score 119.5;	DB 4;	Length 78;	
Best Local Similarity	37.8 %;	Pred. No. 1.6e-05;			
Match count	28.	Conservation score 1.2;	Wormbase+	28.	Trichoplax

Query Match	16	4.8%	Score 119.3,	DB 4;	Length 8;
Best Local Similarity	17	37.8%	Pred. No. 1	1.6e-05;	
Matches	28	Concordant	12;	Mismatched	5;

RESULT	8				
9H293		PRELIMINARY;		PRT;	177 AA.
D	Q9H293				
C	Q9H293;				
T	01-MAR-2001	(TREMBLref.	16,	Created)	
T	01-MAR-2001	(TREMBLref.	16,	Last sequence update)	
T	01-MAR-2001	(TREMBLref.	16,	Last annotation update)	
		INTERPROKIN 17E.			
N		IL17E.			
S	Homo sapiens	(Human).			
C	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
C	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

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[1] N
      SEQUENCE FROM N.A.
      PUBLISHED=11058597;
      X
      Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S., Goddard A.D.; Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.; "IL-17E, a Novel Proinflammatory Ligand for the IL-17 Receptor Homolog IL-17Rhl." J. Biol. Chem. 276:1660-1664 (2001).
      EMBL; AF305200; AAG40848.1; -
      Q
      SEQUENCE 17 AA; 20330 MW; 52D895710CD59871 CRC64;
      Q

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Best Local Similarity	Best Local Score	Best Local Length	Best Local CDS	Best Local Start	Best Local End	Best Local Step	Best Local Gaps
31.58	300	110	CLCRLGCTTGEGEE	1	111	:	1
29	31.58	31	PYRPEAXCLCRLGCTTGEGEE	0.00016	45	111	7

DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	CYTOKINE CX2 PRECURSOR.	
OS	Homo sapiens (Human).	
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homo sapiens (Human); Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBT_TaxID=9606;		
RN	[1]	SEQUENCE FROM N.A.
RA	Zhang W., He L., Wan T., Yuan Z.; Cao X.;	"Novel human cytokine CX2 with homology to IL-17.";
RP	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.	EMBL: AF142410; AAC27921.1; -.
SEQUENCE 197 AA; 21784 MW; BAFB49F631A768 CRC64;		
Query Match 3		
Best Local Similarity 25.7%; Score 187.5; Cao X.;		
Matches 31; Conservative 11; Mismatches 37; Indels 7; Gaps 1;		
QY 17 TNLRSPSPRAYISDPAKPRLPEAVCLRCGLTGLEEDVFRSAPVYMPTVLRR 76		
Db 101 THQRSISPRYRVTDDEDYPOKLAFAECLCRGCDIARTGREDAAALNSVRLQLSSVLRR 160		
QY 77 TPACAGGRSVYTEA-----YVTIPVGCTV 101		
Db 161 RPCSRDGSLPLTPGAFAHTEFIFHPVPGCTV 192		
RESULT 3		
Q9EQ16 PRELIMINARY; PRT; 178 AA.		
ID Q9EQ16; PRT; 178 AA.		
AC O9EQ16; PRT; 178 AA.		
DT 01-MAR-2001 (TREMBLrel. 16, Created)		
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).		
OS Mesocricetus auratus (Golden hamster).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Cricetinae; Mesocricetus.		
NCBI_TaxID=10036;		
RN [1]	SEQUENCE FROM N.A.	
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";		
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Cricetinae; Mesocricetus.		
NCBI_TaxID=10036;		
RN [1]	SEQUENCE FROM N.A.	
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";		
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Cricetinae; Mesocricetus.		
NCBI_TaxID=10036;		
Query Match 24.2%; Score 176.5; DB 11; Length 178;		
Best Local Similarity 42.0%; Pred. No. 3.2e-11; Matches 42; Conservative 9; Mismatches 42; Indels 7; Gaps 2;		
QY 8 PADRRERPP----TNLRSPSPRAYISDPAKPRLPEAVCLRCGLTGLEEDVFR 62		
Db 79 PAKRCEVNLQWLNSKRSPLSPCGYSINHDPSPRIDPLPARCLCLGCVNPFMQDRSM 138		
QY 63 RSAPIVYMPTVLRR--TPACAGGRSVYTEA YVTIPVGCTC 100		
Db 139 VSVPVFESQVPRRLCPPPRSPCRHRYMFTAVGTC 178		
SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;		
RESULT 4		
Q9UHF5 PRELIMINARY; PRT; 180 AA.		
ID Q9UHF5	PRELIMINARY;	PRT; 180 AA.
AC Q9UHF5		
NC Q9UHF5;		
DT 01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE (NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA).		
GN ZCYT07 OR IL20.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NC NCBT_TaxID=9606;		
RN [1]	SEQUENCE FROM N.A.	
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J., Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.		
RN [2]	SEQUENCE FROM N.A.	
RP MEDLINE=0317118; PubMed=10749887;		
RX RA Shi Y., Ulrich R., Connolly K., Grzegorzewski K.J., Zhang J., Barber M.C., Wang W., Watson K., Hodge V., Fisher C.L., Olsen H., Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A., Carroll J.A., Ebner R.; "A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity.";		
RT RT RL J. Biol. Chem. 275:19167-19176(2000).		
RN RN [3]	SEQUENCE FROM N.A.	
RP RX MEDLINE=20105548; PubMed=10639155;		
RA RA Li H., Chen J., Huang A., Stinson J., Heidens S., Foster J., Dowd P., Gurney A.L., Wood W.I.; "Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family.";		
RT RT RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).		
RN RN [4]	SEQUENCE FROM N.A.	
RP RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";		
RT RT RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.		
QY 17 TNLRSPSPRAYISDPAKPRLPEAVCLRCGLTGLEEDVFRSAPVYMPTVLRR 76		
DR DR AF184963; AAF01318.1; -.		
DR DR AF212311; AAF78775.1; -.		
DR DR AF152098; AAF28104.1; -.		
DR DR AF218727; AAG44136.1; -.		
DR DR AF110305; AAG39637.1; -.		
SQ SQ SEQUENCE 180 AA; 20437 MW; FIB0BC1446D0B14A CRC64;		
RESULT 5		
Q9QXT6 PRELIMINARY; PRT; 180 AA.		
ID Q9QXT6	PRELIMINARY;	PRT; 180 AA.
AC Q9QXT6;		
NC Q9QXT6;		
DT 01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE (NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA).		
GN ZCYT07 OR IL20.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NC NCBT_TaxID=9606;		
RN [1]	SEQUENCE FROM N.A.	
RA RA Zhang W., Wang J., Cao X.; "Novel cytokine homology with interleukin-17.";		
RT RT RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.		
QY 17 TNLRSPSPRAYISDPAKPRLPEAVCLRCGLTGLEEDVFRSAPVYMPTVLRR 76		
DR DR AF184963; AAF01318.1; -.		
DR DR AF212311; AAF78775.1; -.		
DR DR AF152098; AAF28104.1; -.		
DR DR AF218727; AAG44136.1; -.		
DR DR AF110305; AAG39637.1; -.		
SQ SQ SEQUENCE 180 AA; 20437 MW; FIB0BC1446D0B14A CRC64;		
Query Match 23.9%; Score 174; DB 4; Length 180;		
Best Local Similarity 43.7%; Pred. No. 6e-11; Matches 9; Mismatches 38; Indels 2; Gaps 38; Conservative		
QY 77 --TPACAGGRSVYTEA YVTIPVGCTC 101		
Db 153 LCPPPPRTGPCRORAVMETIAVGCTC 179		
RESULT 5		
Q9QXT6 PRELIMINARY; PRT; 180 AA.		
ID Q9QXT6	PRELIMINARY;	PRT; 180 AA.
AC Q9QXT6;		
NC Q9QXT6;		
DT 01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DE (NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA).		
GN ZCYT07 OR IL20.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NC NCBT_TaxID=9606;		
RN [1]	SEQUENCE FROM N.A.	
RA Presnell S., Gillett T., Whitmore T., Foster D., Hart C., Lehner J., Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.		
RN [2]	SEQUENCE FROM N.A.	
RP MEDLINE=0317118; PubMed=10749887;		
RX RA Shi Y., Ulrich R., Connolly K., Grzegorzewski K.J., Zhang J., Barber M.C., Wang W., Watson K., Hodge V., Fisher C.L., Olsen H., Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A., Carroll J.A., Ebner R.; "A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity.";		
RT RT RL J. Biol. Chem. 275:19167-19176(2000).		
RN RN [3]	SEQUENCE FROM N.A.	
RP RX MEDLINE=20105548; PubMed=10639155;		
RA RA Li H., Chen J., Huang A., Stinson J., Heidens S., Foster J., Dowd P., Gurney A.L., Wood W.I.; "Cloning and Characterization of IL-17 Cytokine Family.";		
RT RT RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).		
RN RN [4]	SEQUENCE FROM N.A.	
RP RA Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";		
RT RT RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.		
QY 17 TNLRSPSPRAYISDPAKPRLPEAVCLRCGLTGLEEDVFRSAPVYMPTVLRR 76		
DR DR AF184963; AAF01318.1; -.		
DR DR AF212311; AAF78775.1; -.		
DR DR AF152098; AAF28104.1; -.		
DR DR AF218727; AAG44136.1; -.		
DR DR AF110305; AAG39637.1; -.		
SQ SQ SEQUENCE 180 AA; 20437 MW; FIB0BC1446D0B14A CRC64;		
Query Match 23.9%; Score 174; DB 4; Length 180;		
Best Local Similarity 43.7%; Pred. No. 6e-11; Matches 9; Mismatches 38; Indels 2; Gaps 38; Conservative		
QY 93 SNRSLSPWGSYNSNHDPSPRIDPLPARCLCLGCVNPFMQDRSMVSPVPRR 152		
Db 79 PAKRCEVNLQWLNSKRSPLSPCGYSINHDPSPRIDPLPARCLCLGCVNPFMQDRSM 138		
QY 63 RSAPIVYMPTVLRR--TPACAGGRSVYTEA YVTIPVGCTC 100		
Db 139 VSVPVFESQVPRRLCPPPRSPCRHRYMFTAVGTC 178		

	P72236	Pseudomonas					
20	74.5	10.2					
21	74	10.2					
22	73.5	10.1					
23	73.5	10.1					
24	73.5	10.1					
25	72.5	9.9					
26	72	9.9					
27	72	9.9					
28	71.5	9.8					
29	71.5	9.8					
30	71	9.7					
31	70.5	9.7					
32	70.5	9.7					
33	70	9.6					
34	70	9.6					
35	69.5	9.5					
36	69.5	9.5					
37	69.5	9.5					
38	,	9.5					
39	69	9.5					
40	68.5	9.4					
41	68.5	9.4					
42	68.5	9.4					
43	68.5	9.4					
44	68	9.3					
45	68	9.3					
	14.98	11.					
	Q9R57	Q9R57					
	Q9PyC0	Q9PyC0					
	Q9Vx9	Q9Vx9					
	Q9Vpp9	Q9Vpp9					
	Q9Ulv9	Q9Ulv9					
	Q9Ek77	Q9Ek77					
	Q9J157	Q9J157					
	Q9m210	Q9m210					
	Q9fj87	Q9fj87					
	Q9zzf6	Q9zzf6					
	Q9uzK6	Q9uzK6					
	Q9K2B0	Q9K2B0					
	Q9J474	Q9J474					
	Q9Vyx6	Q9Vyx6					
	Q36377	Q36377					
	Q9L777	Q9L777					
	Q9Xav7	Q9Xav7					
	Q9UvM6	Q9UvM6					
	Q9Ptu6	Q9Ptu6					
	Q9J104	Q9J104					
	Q94485	Q94485					
	ALIGNMENTS						
	RESULT	1					
	Q9P0M4	PRELIMINARY;					
	ID Q9P0M4;	PRT;	197 AA.				
	AC						
	DT	01-OCT-2000 [TREMBLrel. 15, Created)					
	DT	01-OCT-2000 [TREMBLrel. 15, Last sequence update]					
	DT	01-OCT-2000 [TREMBLrel. 15, Last annotation update)					
	DE	INTERLEUKIN-17C.					
	OS	Homo sapiens (Human).					
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
	NCBI_TaxID	9606;					
	RN	[1]					
	RP	SEQUENCE FROM N.A.					
	RX	MEDLINE=>20103548; PubMed=10639155;					
	RA	Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,					
	RA	Gurney A.L., Wood W.I.;					
	RA	"Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family."					
	RT	Proc. Natl. Acad. Sci. U.S.A. 97:773-778 (2000).					
	DR	EMBL: AF152099; AAC28105.1; -.					
	SQ	SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7/D08 CRC64;					
	SPTRMBL_16:*						
	1: sp_archaea:*						
	2: sp_bacteria:*						
	3: sp_fungi:*						
	4: sp_human:*						
	5: sp_invertebrate:*						
	6: sp_mammal:*						
	7: sp_mhc:*						
	8: sp_organelle:*						
	9: sp_phage:*						
	10: sp_plant:*						
	11: sp_rhodent:*						
	12: sp_unclassified:*						
	13: sp_vertebrate:*						
	14: sp_virus:*						
	SPTRMBL :						
	1: sp_archaea:*						
	2: sp_bacteria:*						
	3: sp_fungi:*						
	4: sp_human:*						
	5: sp_invertebrate:*						
	6: sp_mammal:*						
	7: sp_mhc:*						
	8: sp_organelle:*						
	9: sp_phage:*						
	10: sp_plant:*						
	11: sp_rhodent:*						
	12: sp_unclassified:*						
	13: sp_vertebrate:*						
	14: sp_virus:*						
	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
	SUMMARIES						
	result	Score	Description				
	No.	Query					
		Match					
		Length					
		DB					
		ID					
	1	187.5	25.7	197	4	Q9P0M4	25.7%; Score 187.5; DB 4; Length 197;
	2	187.5	25.7	197	4	Q9HC75	Best Local Similarity 40.2%; Pred. No. 2.4e-12;
	3	176.5	24.2	178	11	Q9EQ16	Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps .
	4	174	23.9	180	4	Q9UHF5	
	5	173	23.7	180	11	Q9QXT6	
	6	151	20.7	111	1	Q9EQ17	
	7	119.5	16.4	78	4	Q9NU6	
	8	110.5	15.2	177	4	Q9H293	
	9	107.5	14.7	151	14	040633	
	10	99	13.6	148	5	Q19778	
	11	79.5	10.9	520	4	Q9UBG7	
	12	78.5	10.8	226	5	Q9XUH9	
	13	78	10.7	552	4	Q9J723	
	14	78	10.7	805	5	Q9VFD4	
	15	77.5	10.6	1045	6	Q9E545	
	16	76	10.4	242	2	Q9PL24	
	17	75.5	10.4	509	10	Q48780	
	18	75	10.3	178	2	Q9XU01	
	19	75	10.3	242	2	Q84019	
	RESULT	2					
	Q9HC75	PRELIMINARY;					
	ID Q9HC75	PRT;	197 AA.				
	AC						
	DT	01-MAR-2001 [TREMBLrel. 16, Created)					

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Db 282 YASSGGTSLGGSDSPVFEAGVFPQQPAAP 311
 RESULT_15 : ||| | | |
 RRP1_DROME STANDARD; PRT; 1896 AA.
 AC P04052;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6).
 GN RPI1215.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriodea; Drosophilidae; Drosophila.
 RN NCBI_TAXID=7277;
 RP SEQUENCE FROM N.A.
 MEDLINE=89218930; PubMed=2496296;
 RX RA "Analysis of the gene encoding the largest subunit of RNA polymerase II in Drosophila." ;
 RT J. Mol. Gen. Genet. 215:266-275(1989).
 RN [2]
 RP SEQUENCE OF 1-472 FROM N.A.
 RX MEDLINE=8528618; PubMed=2492806;
 RA BIGGS J., Searles L.L., Greenleaf A.L.;
 RT "Structure of the eukaryotic transcription apparatus: features of the gene for the largest subunit of Drosophila RNA polymerase II." ;
 RL Cell 42:611-621(1985).
 RN [3]
 RP SEQUENCE OF 1441-1889 FROM N.A.
 MEDLINE=88094402; PubMed=3122024;
 RA Allison L.A., Wong J.K.-C., Fitzpatrick V.D., Moyle M., Ingles C.J.;
 RT "The C-terminal domain of the largest subunit of RNA polymerase II of Saccharomyces cerevisiae, Drosophila melanogaster, and mammals: a conserved structure with an essential function." ;
 RL Mol. Cell. Biol. 8:321-329(1988).
 CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
 CC -I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + RNA(N).
 CC -I- SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM TEN TO TWELVE DIFFERENT POLYPEPTIDES. THE 215 KDA POLYPEPTIDE IS THE LARGEST COMPONENT OF RNA POLYMERASE II.
 CC -I- SUBCELLULAR LOCATION: NUCLEAR.
 CC -I- PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
 CC THE PHOSPHORYLATION ACTIVATES POL2.
 CC -I- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE mRNA PRECURSOR, AND POLYMERASE III FOR 5S AND tRNA GENES.
 CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
 CC
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 CC
 DR EMBL; M27431; AAA28868; 1; -
 DR EMBL; M11798; AA228863; 1; -
 DR EMBL; M19537; AA228827; 1; -
 DR PIR; S04457; RNPFL;
 DR FlyBase; FBgn000277; RPI1215.
 DR InterPro; IPR000084; -
 DR InterPro; IPR000072; -
 DR InterPro; IPR002879; -

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DR EMBL; AB07919; BAA32295..1; -.

KW Hypothetical protein.

SQ SEQUENCE 425 AA; 43842 MW; 2A6D733CA149E665 CRC64; -.

Query Match 9.8%; Score 71.5; DB 1; Length 425;

Best Local Similarity 34.2%	Pred. No. 3.3;
Matches 26; Conservative 9; Mismatches 26; Indels 15; Gaps 6;	

QY 33 PARYPRYLPEAYCLCRGCHTG ---LFGRF-EDYRFRSAPVY -----MPTVYLLRTPAC 80

DB 326 PERSWRP-PEGACRQGPALQGEMSALFAQKLEETRSKS-PMFSAKGPKLPPCVLPHAFGM 383

QY 81 AG-GRSVYTEAYVTIP 95

DB 384 AGPESPAAAASAWTVSP 399

RESULT 1.3

YMA40_MYCSTRU	STANDARD;	PRT;	265 AA.
ID YMA40_MYCSTRU	STANDARD;	PRT;	265 AA.
AC Q10522;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 30-MAY-2000 (Rel. 39, Last annotation update)			
DE HYPOTHETICAL 27.5 kDa PROTEIN RV2240C.			
GN RV2240C OR MTCY427_21C.			
OS Mycobacterium tuberculosis.			
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;			
OC Actinomycetales; Corynebacterineae; Mycobacterium.			
OX NCBI_TAXID=1773;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN:H37RV;			
RX MEDLINE:98295987; PubMed:96342230;			
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Biggheimer K., Gas S., Barry C.E. III, Tekai F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hollroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutten S., Seeger K., Shelton S., Squares S., Strelkowa N., Taylor K., Whitehead S., Barrell B.G.;			
RA *Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. ";			
RA Nature 393:537-544 (1998).			
CC DR EMBL; Z70592; CAA04661..1; -.			
CC DR TuberoulList; Rv2240c; -.			
CC KW Hypothetical protein; Transmembrane.			
CC FT TRANSMEM 89 109 MW; F9E7ACF5A736B90A CRC64; -.			
CC SQ SEQUENCE 27529 AA; 27529 MW; F9E7ACF5A736B90A CRC64; -.			

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CC DR EMBL; Li2319; AAC05819..1; -.

CC DR InterPro; IPR000571; -.

CC DR Pfam; PF00642; zf-CCCH; 2.

CC KW Nuclear protein; Repeat; Zinc-finger; Zinc-binding; Zinc-finger; DNA-binding.

CC FT REPEAT 69 73 P-P-P-G.

CC FT REPEAT 196 200 P-P-P-G.

CC FT REPEAT 218 222 P-P-P-G.

CC FT ZNFING 107 126 CX (8)CX (5)CX (3)H-TYPE.

CC FT ZNFING 145 164 CX (8)CX (5)CX (3)H-TYPE.

CC SQ SEQUENCE 324 AA; 34087 MW; 60460579EA278EE CRC64; -.

Db 24 ACCLDGRPPIVPHRRRRITAALRSVLRLRDTPRPARSRCDQVTSHAVLJIGWRAVPRRGG 83

QY 39 YLPBAYCLCRGC ---LTGLFGEEDVRL ---FRSAPVYMPMTVVLRRTPACAGG --- 83

Db 84 ELPRGAAHALGCTALLINGIVGCTTWTGTAMPDTNVAPYRSSVSVASASATSSIRE 143

QY 84 ---RSVYTEAYVTIPVGCTCYCEPEKDA-DSINSSTDQAKLLGGNDAPA 131

Db 144 SQRQQLSTKA --IRTSCLDLATAKSQAKDIAKYNAVAFNQGRNTGTGEGPA 193

RESULT 14

TTP_BOVIN	STANDARD;	PRT;	324 AA.
ID TTP_BOVIN	STANDARD;	PRT;	324 AA.
AC P53781			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 01-OCT-2000 (Rel. 40, Last annotation update)			
DE TRISTRITETAPROLINE (TTP) (TIS11A PROTEIN) (TIS11) (ZFP-36).			
OS Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea; Bovidae; Bovinae; Bos.			
OC NCBITaxID=9913;			
OX [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=liver;			
RX MEDLINE=96027638; PubMed=7559666;			
RA Lai W.S., Thompson M.J., Taylor G.A., Liu Y., Blackshear P.J.; RT "Promoter analysis of zfp-36, the mitogen-inducible gene encoding the zinc finger protein tristrataprolin." RL J. Biol. Chem. 270:25266-25272(1995).			
CC -1- FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER STRUCTURE INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.			
CC HAS BEEN EXPERIMENTALLY SHOWN TO BE ABLE TO BIND ZINC.			
CC -1- SUBCELLULAR LOCATION: NUCLEAR.			
CC -1- INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.			
CC -1- SIMILARITY: CONTAINS 2 CX (8)CX (5)CX (3)H-TYPE ZINC FINGERS.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC DR EMBL; Li2319; AAC05819..1; -.			
CC DR InterPro; IPR000571; -.			
CC DR Pfam; PF00642; zf-CCCH; 2.			
CC KW Nuclear protein; Repeat; Zinc-finger; Zinc-binding; Zinc-finger; DNA-binding.			
CC FT REPEAT 69 73 P-P-P-G.			
CC FT REPEAT 196 200 P-P-P-G.			
CC FT REPEAT 218 222 P-P-P-G.			
CC FT ZNFING 107 126 CX (8)CX (5)CX (3)H-TYPE.			
CC FT ZNFING 145 164 CX (8)CX (5)CX (3)H-TYPE.			
CC SQ SEQUENCE 324 AA; 34087 MW; 60460579EA278EE CRC64; -.			
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Best Local Similarity 28.0%; Pred. No. 3.9;			
Matches 42; Conservative 10; Mismatches 51; Indels 47; Gaps 9;			
QY 6 GRPADRRFR-PPTPLR--SVSPWARYSITDPARYPRYL---PEAYCUCRGCL/GLFGEED 59			
Db 187 GLPSGRRTSPSPASLAGPSWSFSPPSPSSPPPGDILLSPSA----- 230			
QY 60 VRFRSAPVYMPMTVLLR - TPACAGGRSYTEAVTIPGCTCYPEPEKDADSINNSIDK 117			
Db 231 -FSRAPGHL---CRDPTPACCPSCRRATPNWSVWGVGGLA --RSPSAHSUJGSDPDE 281			
QY 118 ---OGAKL-----LLGPNDAPAGP 133			

DE (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M).
 GN CSP2.
 OS MUS musculus (Mouse).
 OC Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
 OC Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
 OC Hyaluronic acid; Alternative splicing.
 OC POTENTIAL.
 OC VERSICAN CORE PROTEIN.
 OC IG-LIKE V-TYPE DOMAIN.
 [1] RQ SEQUENCE FROM N.A. (VARIANTS V0; V1 AND V2).
 RC STRAIN=CS7BL/6; AND SWISS WEBSTER; TISSUE=brain;
 RX MEDLINE=9512551; PubMed=7822336;
 RA Ito K., Shinomura T., Zako M., Ujita M., Kimata K.;
 RA "Multiple forms of mouse PG-M, a large chondroitin sulfate
 proteoglycan generated by alternative splicing.";
 RT J. Biol. Chem. 270:958-965 (1995).
 [2] RQ SEQUENCE OF 1-348 AND 3053-3358 FROM N.A. (VARIANT V3).
 RC STRAIN=CS7BL/6;
 RX MEDLINE=95181355; PubMed=7876137;
 RA Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
 RA "Expression of PG-M(V3), an alternatively spliced form of PG-M
 without a chondroitin sulfate attachment in region in mouse and human
 tissues.";
 RT J. Biol. Chem. 270:3914-3918 (1995).
 CC -I- FUNCTION: MAY PLAY A ROLE IN INTERCELLULAR SIGNALING AND IN
 CC CONNECTING CELLS WITH THE EXTRACELLULAR MATRIX. MAY TAKE PART IN
 CC THE REGULATION OF CELL MOTILITY, GROWTH AND DIFFERENTIATION. BINDS
 CC HYALURONIC ACID.
 CC -I- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX.
 CC -I- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; V0 (SHOWN HERE), V1,
 CC V2 AND V3; ARE PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- TISSUE SPECIFICITY: V2 IS FOUND ONLY IN BRAIN.
 CC -I- DEVELOPMENTAL STAGE: DISAPPEARS AFTER THE CARTILAGE DEVELOPMENT.
 CC -I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -I- SIMILARITY: CONTAINS 2 LINK DOMAINS.
 CC -I- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
 CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -I- SIMILARITY: CONTAINS 1 SUSHI (SCR) REPEAT.
 CC -I- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.

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CC EMBL: D16263; BAA03796.1; -.
 DR EMBL: D28599; -; NOT_ANNOTATED_CDS.
 DR EMBL: D32040; BAA06802.1; -.
 HSSP: P00740; LIXA.
 DR MGD: MG1:102889; Cspg2.
 DR InterPro: IPR001452; -.
 DR InterPro: IPR000436; -.
 DR InterPro: IPR000538; -.
 DR InterPro: IPR000561; -.
 DR InterPro: IPR001304; -.
 DR InterPro: IPR001438; -.
 DR InterPro: IPR001881; -.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00193; Link; 2.
 DR Pfam: PF00047; Ig; 1.
 DR PROSITE: PS00022; EGF-1; 2.
 DR PROSITE: PS00186; EGF-2; 1.
 DR PROSITE: PS01187; EGF CA; 1.
 DR PROSITE: PS01241; Link; 2.
 DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.

Query Match 54 10.0% Score 73; DB 1; Length 3358;
 Best Local Similarity 32.1%; Pred. No. 24; Mismatches 10; Indels 33; Gaps 4;
 Matches 26; Conservative 10; Nmatches 33; Indels 12; Gaps 1;

Qy LFGBEDVFRSAPYMPTVLRLTPACAGGRSYV-TE-AYVTLPGVCTCP-----EPEK 106
 Db 3035 LIGISESESVETAVYLPGPDLCNKINPLNGTCPTERTSYV---CFCAPGYSQDQCEL 3089

Qy 107 DADSINSSDKQGAKILLGPN 127
 Db 3090 DFDECHSNPCRNGATCVDFGN 3110

RESULT 11
 CDN1_HUMAN
 ID CDN1_HUMAN
 AC P38336;
 DT 01-FEB-1995 (Rel. 31, Created)

CC -1- FUNCTION: RECEPTOR FOR COMPLEMENT C3D AND FOR THE EPSTEIN-BARR VIRUS ON HUMAN B-CELLS AND T-CELLS. PARTICIPATES IN B LYMPHOCYTES ACTIVATION.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPlicing.

CC -1- TISSUE SPECIFICITY: MATURE B LYMPHOCYTES, T LYMPHOCYTES AND FOLLICULAR DENDRITIC CELLS OF THE SPLEEN.

CC -1- SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.

CC -1- SIMILARITY: CONTAINS 15 SUSHI (SCR) DOMAINS.

CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD21 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd21.htm".

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DR EMBL; M26004; AAA35786.1; -.

DR EMBL; M26016; AAB04638.1; -.

DR EMBL; M24007; AAB04638.1; JOINED.

DR EMBL; M24008; AAB04638.1; JOINED.

DR EMBL; M24009; AAB04638.1; JOINED.

DR EMBL; M24010; AAB04638.1; JOINED.

DR EMBL; M24011; AAB04638.1; JOINED.

DR EMBL; M26009; AAB04638.1; JOINED.

DR EMBL; M26010; AAB04638.1; JOINED.

DR EMBL; M26011; AAB04638.1; JOINED.

DR EMBL; M26012; AAB04638.1; JOINED.

DR EMBL; M26013; AAB04638.1; JOINED.

DR EMBL; M26014; AAB04638.1; JOINED.

DR EMBL; M26015; AAB04638.1; JOINED.

DR EMBL; S62896; AAB227186.1; -.

DR PIR; A32036; A32036.

DR PIR; A24319; A24319.

DR PIR; C24319; C24319.

DR PIR; D24319; D24319.

DR PIR; E24319; E24319.

DR PIR; F24319; F24319.

DR HSSP; P1098; IVVC.

MIM; 120650; -.

DR InterPro; IPR000436; -.

Pfam; PF00084; sushi; 15.

Complement pathway; Glycoprotein; Transmembrane; Repeat; Signal;

KW Receptor; Sushi; Alternative splicing.

FT SIGNAL 1 20

FT CHAIN 21 1033

FT DOMAIN 21 971

FT TRANSMEM 972

FT DOMAIN 1000 1033

FT DOMAIN 22 83

FT DOMAIN 90 147

FT DOMAIN 153 211

FT DOMAIN 214 272

FT DOMAIN 275 343

FT DOMAIN 350 407

FT DOMAIN 409 467

FT DOMAIN 470 523

FT DOMAIN 526 594

FT DOMAIN 601 658

FT DOMAIN 661 715

FT DOMAIN 718 780

FT DOMAIN 787 844

FT DOMAIN 850 908

FT DOMAIN 911 969

FT DISULFID 23 65

FT DISULFID 51 82

FT DISULFID 91 132

CC ACTIVATION. BY SIMILARITY.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BY SIMILARITY.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPlicing. BY SIMILARITY.

CC -1- TISSUE SPECIFICITY: MATURE B LYMPHOCYTES, T LYMPHOCYTES AND FOLLICULAR DENDRITIC CELLS OF THE SPLEEN. BY SIMILARITY.

CC -1- SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA) FAMILY. BY SIMILARITY.

CC -1- SIMILARITY: CONTAINS 15 SUSHI (SCR) DOMAINS. BY SIMILARITY.

CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD21 entry; BY SIMILARITY.

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd21.htm". BY SIMILARITY.

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DR EMBL; M26004; AAA35786.1; -.

DR EMBL; M26016; AAB04638.1; -.

DR EMBL; M24007; AAB04638.1; JOINED.

DR EMBL; M24008; AAB04638.1; JOINED.

DR EMBL; M24009; AAB04638.1; JOINED.

DR EMBL; M24010; AAB04638.1; JOINED.

DR EMBL; M24011; AAB04638.1; JOINED.

DR EMBL; M26009; AAB04638.1; JOINED.

DR EMBL; M26010; AAB04638.1; JOINED.

DR EMBL; M26011; AAB04638.1; JOINED.

DR EMBL; M26012; AAB04638.1; JOINED.

DR EMBL; M26013; AAB04638.1; JOINED.

DR EMBL; M26014; AAB04638.1; JOINED.

DR EMBL; M26015; AAB04638.1; JOINED.

DR EMBL; S62896; AAB227186.1; -.

DR PIR; A32036; A32036.

DR PIR; A24319; A24319.

DR PIR; C24319; C24319.

DR PIR; D24319; D24319.

DR PIR; E24319; E24319.

DR PIR; F24319; F24319.

DR HSSP; P1098; IVVC.

MIM; 120650; -.

DR InterPro; IPR000436; -.

Pfam; PF00084; sushi; 15.

Complement pathway; Glycoprotein; Transmembrane; Repeat; Signal;

KW Receptor; Sushi; Alternative splicing.

FT SIGNAL 1 20

FT CHAIN 21 1033

FT DOMAIN 21 971

FT TRANSMEM 972

FT DOMAIN 1000 1033

FT DOMAIN 22 83

FT DOMAIN 90 147

FT DOMAIN 153 211

FT DOMAIN 214 272

FT DOMAIN 275 343

FT DOMAIN 350 407

FT DOMAIN 409 467

FT DOMAIN 470 523

FT DOMAIN 526 594

FT DOMAIN 601 658

FT DOMAIN 661 715

FT DOMAIN 718 780

FT DOMAIN 787 844

FT DOMAIN 850 908

FT DOMAIN 911 969

FT DISULFID 23 65

FT DISULFID 51 82

FT DISULFID 91 132

CC ACTIVATION. BY SIMILARITY.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. BY SIMILARITY.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPlicing. BY SIMILARITY.

CC -1- TISSUE SPECIFICITY: MATURE B LYMPHOCYTES, T LYMPHOCYTES AND FOLLICULAR DENDRITIC CELLS OF THE SPLEEN. BY SIMILARITY.

CC -1- SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA) FAMILY. BY SIMILARITY.

CC -1- SIMILARITY: CONTAINS 15 SUSHI (SCR) DOMAINS. BY SIMILARITY.

CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD21 entry; BY SIMILARITY.

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd21.htm". BY SIMILARITY.

FT DISULFID 118

FT DISULFID 154

FT DISULFID 210

FT DISULFID 215

FT DISULFID 242

FT DISULFID 276

FT DISULFID 305

FT DISULFID 351

FT DISULFID 393

FT DISULFID 379

FT DISULFID 406

FT DISULFID 410

FT DISULFID 439

FT DISULFID 509

FT DISULFID 495

FT DISULFID 527

FT DISULFID 556

FT DISULFID 593

FT DISULFID 602

FT DISULFID 630

FT DISULFID 662

FT DISULFID 685

FT DISULFID 719

FT DISULFID 762

FT DISULFID 779

FT DISULFID 798

FT DISULFID 830

FT DISULFID 843

FT DISULFID 851

FT DISULFID 880

FT DISULFID 912

FT DISULFID 941

FT CARBOHYD 121

FT CARBOHYD 127

FT CARBOHYD 294

FT CARBOHYD 372

FT CARBOHYD 492

FT CARBOHYD 623

FT CARBOHYD 682

FT CARBOHYD 800

FT CARBOHYD 823

FT CARBOHYD 861

FT CARBOHYD 911

FT VARSPLIC 499

FT VARSPLIC 525

FT VARSPLIC 556

FT PCPYPVYNGAHTGSSLEDFPYGTTVYTC -> NHLPPT

ISOPFORM).

FT CONFLICT 667

FT CONFLICT 902

FT CONFLICT 906

FT SEQUENCE 1033 AA; 112973 MW; 1749DB4A07847ADA CRC64;

Query Match 10.1%; Score 73.5%; DB 1; Length 1033;

Best Local Similarity 25.0%; Pred No. 5; 5;

Matches 32; Conservative 8; Mismatches 41; Indels 47; Gaps 5;

Qy 15 PPTNLRLRSVPWARYSPDARYPRYLPEAYCYLCRGCLTG -LFGEEEDYFRSAPVYMPV 72

Db 413 PPNLNGOKEDRMRMVRDEGTISKY-----SCNFGVVLGEESTQCTSEGWNTPPV 463

Qy 73 VLRRTPAC-AGGR-----SYTEAVYTIP-----

Db 464 PQCKVAEATGRQLLKPKHQFVRPDVNSCCGEGYKLGSVYQECDCITPWFMEIRLCK 523

Qy

Db 524 EITCPCPP 531

RESULT 10

PGCV_MOUSE STANDARD; PRT; 3358 AA.

ID PGCV_MOUSE ID: 1: 1

AC 062059; 062058; DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN)

Db	151	LGRQAAK	157
RESULT	6	A2HS_PIG	
ID	A2HS_PIG	STANDARD;	PRT; 362 AA.
AC	P29700;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) (FRAGMENT).		
GN	AHSG OR FETUA.		
OS	Sus scrofa (Pig).		
OU	Eukaryota; Metazoa; Chordata; Craniata; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviaria; Sus.		
NCBI_TaxID	9823;		
OX	[1]		
RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RP	TISSUE-Liver;		
RC	MEDLINE-92209519; PubMed-11372866;		
RX	Brown W.M., Christie D.L., Saunders N.R., Nawratil P., Dziedielewska K.D., Mueller-Bsterl W.		
RA	"The nucleotide and deduced amino acid structures of sheep and pig fetuin. Common structural features of the mammalian fetuin family.";		
RA	Eur. J. Biochem. 205:321-331(1992).		
RT	-1 SUBCELLULAR LOCATION: SECRETED.		
CC	-1 SIMILARITY: BELONGS TO THE FETUIN FAMILY.		
CC	-1 SIMILARITY: CONTAINS 2 CYSTATIN-LIKE DOMAINS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL; X56021; CAA39498.1; -.		
CC	PIR; S22142; S22395; S22395.		
CC	InterPro; IPRO00010;		
CC	DR		
CC	PFam; PF00031; cystatin; 2.		
CC	DR		
CC	PROSITE; PS01154; FETUIN_1; 1.		
CC	DR		
CC	PROSITE; PS01255; FETUIN_2; 1.		
CC	KW		
CC	Glycoprotein; Signal; Repeat.		
CC	NON-TER	1	
CC	FT	SIGNAL	<1
CC	FT	CHAIN	15
CC	FT	DOMAIN	16
CC	FT	DISULFID	16
CC	FT	DISULFID	24
CC	FT	DISULFID	142
CC	FT	DISULFID	29
CC	FT	DISULFID	1
CC	FT	DISULFID	15
CC	FT	DISULFID	16
CC	FT	DISULFID	205
CC	FT	DISULFID	227
CC	FT	CARBONYD	244
CC	FT	CARBONYD	96
CC	FT	CARBONYD	153
CC	FT	CARBONYD	173
CC	SEQUENCE	362 AA;	38424 MW;
CC			532648EEA34B5686 CRC64;
CC			
CC	Query Match	10.38%	Score 75; DB 1; Length 362;
CC	Best Local Similarity	27.6%	pred. No. 1.2;
CC	Matches 27;	Conservative 11;	Mismatches 42; Indels 18; Gaps 3;
CC	30 SYDPARYPRYLPEAYCLCRCLGLFGEEEDYFRSAPVYMPYVYLRRTPACAGGRSYVTE 89		
CC	210 AYSPKCNLLEVKQFGKGTVAKVNEEDAVICTVFQTQPVVLQQPAGA----- 261		
Qy			
Db			

versican precursor - mouse
 N: Alternative names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
 versican

N: Contains: glial hyaluronate-binding protein

C: Species: Mus musculus (house mouse)

C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 # text_change 10-Sep-1999

C: Accession: A55335

R: Ito, K.; Shinonoura, T.; zako, M.; Ujita, M.; Kimata, K.

J. Biol. Chem. 270, 9879-965, 1995

A: Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate

A: Reference number: A55335; MUID:95122551

A: Accession: A55335

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 1-2397 <RES>

A: Cross references: GB:D16263; NID:9862460; PID:BA003796.1; PID:9862461

C: Superfamily: versican; c-type lectin homology; complement factor H repeat homology; EC

F: 1-20/Domain: signal sequence #status predicted <STIG>

F: 21-1654/Domain: versican #status predicted <MAT>

F: 167-244/Domain: link protein repeat homology <LNK2>

F: 265-346/Domain: link protein repeat homology <LNK1>

F: 2095-2126/Domain: EGF homology <EG1>

F: 2133-2164/Domain: EGF homology <EG2>

F: 2171-2291/Domain: C-type lectin homology <LCH>

F: 2298-2354/Domain: complement factor H repeat homology <FHHD>

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 1-181 <RES>

A: Cross references: GB:L47233; NID:9986878; PID:AA859560.1; PID:9986879

C: Accession: 168674; A49437; T54142; S39357

R: Rousses, S.; Orcelik, H.; Lee, P.D.; Maikin, D.; Bull, S.B.; Andrusis, I.L.

Hum. Mol. Genet. 4, 1089-1092, 1995

A: Title: Two variants of the CIP1/WAF1 gene occur together and are associated with human

A: Reference number: 154380; MUID:95384154

A: Accession: 168674

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 1-181 <RES>

A: Cross references: GB:L26165; NID:9418017; PID:AA19811.1; PID:9433742

R: Xiong, Y.; Hannan, G.J.; Zhang, H.; Casso, D.; Kobayashi, R.; Beach, D.

N: Contains: a universal inhibitor of cyclin kinases .

A: Title: p21 is a universal inhibitor of cyclin kinases .

A: Accession: S39357; MUID:94081955

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 18-181 <XTO>

A: Cross references: GB:S67388; NID:9453134; PID:AA829246.1; PID:9453135

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A: Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi

A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L47233; NID:9986878; PID:AA859560.1; PID:9986879

R: Harper, J.W.; Adami, G.R.; Wei, N.; Keyomarsi, K.; Elledge, S.J.

Cell 75, 805-816, 1993

A: Title: The p21 Cdk-interacting protein Cip1 is a potent inhibitor of G1 cyclin-dependen

A: Reference number: A19437; MUID:94061996

A: Accession: A49437

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES3>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Harper, J.W.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A: Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi

A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A: Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi

A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Molecule type: mRNA

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A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Status: preliminary; translated from GB/EMBL/DDJB

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A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A: Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi

A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

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A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

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A: Reference number: 15412; MUID:94170884

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A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

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A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A: Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi

A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; venable, S.F.; Pereira-Smith, O.M.; Smith, J.R.

Exp. Cell Res. 211, 90-98, 1994

A: Title: Cloning of senescent cell-derived inhibitors of DNA synthesis using an expressi

A: Reference number: 15412; MUID:94170884

A: Accession: 153412

A: Status: preliminary; translated from GB/EMBL/DDJB

A: Molecule type: mRNA

A: Residues: 18-181 <RES2>

A: Cross references: GB:L25610; NID:9425142; PID:AA16109.1; PID:9425143

R: Noda, A.; Ning, Y.; ven

A71568 hypothetical protein CT016 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C;Species: Chlamydia trachomatis
 C;Accession: A71568 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282: 754-759, 1998
 A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A;Reference number: A71570; MUID:99000809
 A;Accession: A71568
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-242 <ARN>
 A;Cross-references: GB:AE001276; GB:AE001273; NID:93328399; PIDN: AAC67606.1; PID:9332840
 A;Experimental source: serotype D, strain UW-3/Cx
 C;Genetics:
 A;Gene: CT016 .

Query Match Score 10.3%; DB 2; Length 242;
 Best Local Similarity 25.0%; Pred. No. 2.1; Gaps 3;
 Matches 20; Conservative 7; Mismatches 21; Indels 32; Gaps 3;

```

Qy 41 PRAYCLRGCLTGL-----FGEEDVRRPASAPYMPMTVLLRTPACAGRSVYT--- 88
Db 161 PRPHCNCNLHCQIGRATVEEDAGVSDEDDLTFRSVDI-----SQSGEKMYTVTD 208
Qy 89 -----EAVTTIPVGCTC 100
Db 209 PLNPEEOFNVYLGTPIGCTC 228

```

RESULT 11
 fetuin precursor - pig (fragment),
 C;Species: sus scrofa domestica (domestic pig)
 C;Accession: S22395; S22142
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
 R;Brown, W.M.; Dziegielewska, K.M.; Saunders, N.R.; Christie, D.L.; Nawratil, P.; Muelle Eur. J. Bioch. 205, 321-331, 1992
 A;Title: The nucleotide and deduced amino acid structures of sheep and pig fetuin. Command
 A;Reference number: S22394; MUID:92209519
 A;Accession: S22395
 A;Molecule type: mRNA
 A;Residues: 1-362

 C;Cross-references: EMBL:X56021; NID:92104; PIDN:CAA39498.1; PID:93980229
 C;Superfamily: alpha-2-HS-glycoprotein; cystatin homology
 C;Keywords: calcium binding; EF hand; glycoprotein
 F;1-15-/Domain: signal sequence (fragment) #status predicted <SIG>
 F;16-362-/Product: fetuin #status predicted <MAT>
 F;20-134-/Domain: cystatin homology <CY1>
 F;143-249-/Domain: cystatin homology <CY2>
 F;96-153,173-/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 10.3%; DB 2; Length 362;
 Best Local Similarity 27.6%; Pred. No. 3.3; Gaps 3;
 Matches 27; Conservative 11; Mismatches 42; Indels 18; Gaps 3;

```

Qy 30 SYDPARYPRYLPEAYCLCRGCLTGIFGEEDVRRPASAPYMPMTVLLRTPACAGRSVYT 89
Db 210 ASPTICNLLYEKQYGFCKGPTVAKYNEEDVAVTCVFTQTOPVVLQPQPCA----- 261
Qy 90 AWVTIPVGCTCPEPERKADATNSSSI-DKGAKLILGP 126
Db 262 ----DAGAT----PVYDAATAASPLADVPRAASLVGP 290

```

RESULT 12
 S28941 coagulation factor XIa (EC 3.4.21.38) - guinea pig (fragment)
 N;Alternate names: Hageman factor
 C;Species: Cavia porcellus (guinea pig)

C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 R;Semb, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, Biochim. Biophys. Acta 1159, 113-121, 1992
 A;Title: Primary structure of guinea pig Hageman factor: sequence around the cleavage site
 A;Reference number: S28941; MUID:93003367
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-603 <SEM>
 A;Cross-references: EMBL:X68615; NID:949578; PIDN:CAA48600.1; PID:g49579
 C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolog
 C;Keywords: hydrolase; serine proteinase
 F;46-87-/Domain: fibronectin type II repeat homology <FB1>
 F;177-208-/Domain: EGF homology <EGF>
 F;216-294-/Domain: kringle homology <KRG>
 F;359-597-/Domain: trypsin homology <TRY>

Query Match Score 10.3%; DB 2; Length 603;
 Best Local Similarity 22.2%; Pred. No. 5.7; Gaps 7;
 Matches 37; Conservative 17; Mismatches 59; Indels 54; Gaps 7;

```

Qy 2 CPAGGRPADRRRFRPPT-NLRSPVSPRAYSTDPARYPRY-----LPEAY 44
Db 60 CTHKGRCGRPMCATPFDQQWYCL--EPKKVYDHCSKHNPCQRGGICVNTLSSPH 117
Qy 45 CLCRGCLTG-----LGEDYDVRFSAPV-----YMPTVL 74
Db 118 CLCPDHLTGKHCQREKCFCFEPOLHRFHENELWFRTPGAVKCHCKGPDAHKQMHQSQC 177
Qy 75 RRTPACAGGRSVYTEAV-----VTPVGCTCVPEPEKDADSINSIDKOG 119
Db 178 QTNPCLNLNGRCLEVEHHLCDCPMGTY---GPFCDLDTATSCYEGRC 221

```

RESULT 13
 T38292 hypothetical protein SPAC23E2.02 - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Accession: T38292 #sequence_revision 03-Dec-1999
 R;Skelton, J.; Churcher, C. M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, January 1996
 A;Reference number: Z21784
 A;Accession: T38292
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1273 <SKER>
 A;Cross-references: EMBL:Z68887; PIDN:CAA93114.1; GSPDB:GN00066; SPDB:SPAC23E2.02
 A;Experimental source: strain 972h-; cosmid c23E2
 C;Genetics:
 A;Gene: SPAC23E2.02
 A;Map position: 1
 A;Introns: 8/2; 862/3

Query Match Score 10.2%; DB 2; Length 1273;
 Best Local Similarity 25.6%; Pred. No. 15; Gaps 1;
 Matches 22; Conservative 15; Mismatches 48; Indels 1; Gaps 1;

```

Qy 46 LCRGCCLTGIFGEEDVRRPASAPYMPMTVLLRTPACAGRSVYT 105
Db 520 ICARQITGLFSEYSSFLSKNELPPKVILEAKERTGGR-TYSRALPVSHTSATOINHHT 578
Qy 106 KDADSLNSIDKQGAKLILGPNDAPA 131
Db 579 SNSNSISSNSTSLNPRTDSDHIPS 604

```

RESULT 14
 A55535

C;Accession: B81719
 R;Residues: T.D.; Bruntam, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255
 A;Accession: B81719
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-242 <TET>
 A;Cross-references: GB:AE002296; GB:AE002160; NID:97190325; PIDN:AAF39152.1; PID:J719032
 A;Experimental source: strain Niigg (MoPn)
 C;Genetics:
 A;Gene: TC0284

Query Match 10.4%; Score 76; DB 2; Length 242;
 Best Local Similarity 26.2%; Pred. No. 1.7; Gaps 3;
 Matches 21; Conservative 6; Mismatches 21; Indels 32; Gaps 3;

QY 41 PEAYCLCRGCLTGLF-----GEEDYRFRSAPVYMPVTYVLRRTPACAGGRSYVTT--- 88
 DB 161 PEPHCNLCLCQIGRIAVEPBDIESEEDLTFRSWDI-----SQYGERMYTVTD 208

QY 89 -----EAYVTPVGCTC 100
 DB 209 PLNPEEFQFNVLGPIGCTC 228

RESULT 7
 A84663
 C;Species: Arabidopsis thaliana [imported] - Arabidopsis thaliana
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Accession: A84420; MUID:20083487
 A;Reference number: A84420; MUID:20083487
 A;Accession: A84663
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-509 <STO>
 A;Cross-references: GB:AE002093; NID:92760030; PIDN:AAK95298.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g26640
 A;Map position: 2

Query Match 10.4%; Score 75.5%; DB 2; Length 509;
 Best Local Similarity 31.3%; Pred. No. 4.2; Gaps 5;
 Matches 26; Conservative 16; Mismatches 28; Indels 13; Gaps 5;

QY 48 RGCLTGLFEEEDYRFRSAPVYMPVTYVLRRTPACAGGRSYV-TAYVTPVGCTCVPPEPK 106
 DB 124 RSKLTGSFTEENLEFQRK-----ILQRSGL---GESTYLEAVLNYPNP-PCMKEARK 172

QY 107 DADSN-SSIDKQAKLLGPND 128
 DB 173 EAETVMFGAIDELLAKTNNPKD 195

RESULT 8
 T44254
 thiamin biosynthesis protein thiC [imported] - Rhizobium etli plasmid b
 C;Species: Rhizobium etli
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 R;Miranda-Rios, J.; Moreira, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sol J. Bacteriol. 179, 6887-6893, 1997
 A;Title: Expression of thiamin biosynthetic genes (thiCOGE) and production of symbiotic

A;Reference number: 222737; MUID:98037482
 A;Accession: T44254
 A;Status: preliminary; translated from GB/EMBL/DDBU
 A;Molecule type: DNA
 A;Residues: 1-610 <MR>
 A;Cross-references: EMBL:AF004408; NID:92627325; PIDN:AAC45972.1; PID:q2627326
 A;Experimental source: strain CE3
 C;Genetics:
 A;Gene: thiC
 A;Genome: Plasmid b
 C;Function:
 A;Description: involved in the biosynthesis of the pyrimidine moiety of thiamin
 C;Superfamily: thiamin biosynthesis protein thiC

Query Match 10.4%; Score 75.5%; DB 2; Length 610;
 Best Local Similarity 29.9%; Pred. No. 5.1; Gaps 7;
 Matches 38; Conservative 14; Mismatches 54; Indels 21; Gaps 7;

QY 3 PAGGRPADRRERPTNLRSVSPW--AYRISYPARYLPAYCLRGCLTGLFGE-- 57
 DB 44 PTGEGP----PVTVIYSSGPTDPAVISID-AGLR-LRBSWIKRGDVESYDGIV 95

QY 58 --EDYRFRSAPVYMPVTYVLRRTPACA-GGRSYVTEAYVTPVGCTCVPPEPKDADINNS 114
 DB 96 KPEDNGFATGERLTPEFFVRNTPLAKAGRATVQLAYAR----AGTVTPMEMFIA TREN 150

QY 115 IDKQAK 121
 DB 151 LGRQAAK 157

RESULT 9
 D72281
 hypothetical protein TM1214 - Thermotoga maritima (strain MSBB)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C;Accession: D72281
 R;Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M. Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A;Accession number: A72200; MUID:99288316
 A;Accession: D72281
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-178 <ARN>
 A;Cross-references: GB:AE001778; GB:AE000512; NID:94981757; PIDN:AA036289.1; PID:q498
 A;Experimental source: strain MSBB
 C;Genetics:
 A;Gene: TM1214
 C;Superfamily: psbG protein

Query Match 10.3%; Score 75%; DB 2; Length 178;
 Best Local Similarity 23.1%; Pred. No. 1.5; Gaps 7;

Matches 34; Conservative 12; Mismatches 35; Indels 66; Gaps 7;

QY 18 NLRSVSPWAVRISYPARYLPAYCLRGC-----LNGLFGEEDVFRPSAPV-- 67
 DB 13 NLRSRSTWMLH-----YCTGGCAVELPPSMTSRFDEME-RFGIAPMAT 53

QY 68 -----YMTVYVQRT-----PACAGGRSRVYMEAYVT----- 93
 DB 54 PRODILILITGYLNKTKLRRVITYEQMDPKVYVGFSCTINGIYFDSYATVNRLDYY 113

QY 94 IPVG---CTCVPEPEKDAIDSINSSDK 117
 DB 114 IPDVVIAGCMRPEALFEANVLMEK 140

RESULT 10

A;Residues: 1-151 <NIC>
A;Cross references: GB:M60286; NID:g331040; PIDN:AAA46156.1; PID:9331042
R;Albrecht, J.
Submitted to the EMBL Data Library, January 1992
A;Description: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A36806
A;Accession: D36807
A;Molecule type: DNA
A;Residues: 1-151 <ALB>
A;Cross references: GB:X64346; NID:g60320; PIDN:CAA5636.1; PID:gg60334
R;Albrecht, J.C.; Nicholas, J.J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Wi
J. Virol. 66, 5047-5058, 1992
A;Title: Primary structure of the herpesvirus saimiri genome.
A;Reference number: A37309; MUTD:92333688
A;Contents: annotation; protein-coding frames
A;Note: neither protein nor nucleotide sequence is given
C;Genetics:
A;Gene: 13
C;Superfamily: saimiri herpesvirus immediate-early protein 2
C;Keywords: early protein

Query Match 14.9% Score 108.5; DB 1; Length 151;
Best Local Similarity 31.4%; Pred. No. 0.0039;
Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

QY 20 RSVSPWAXRISDPARYPRLYPEAYCLCRGCLTGLFGEEDDVFRSAPVYMPVTLRRTPA 79
DB 65 RSTSPWTLHRNEDQDRTPSIVIWEAKCRYLGMNSVPTIQQEELVVRK--- 120

QY 80 CAGRSVTEAY ---VTPVGTCV 101
DB 121 --GHQPCPNSSFRLEKMLVTVGCTCV 143

RESULT 3
199623
cytotoxic T-lymphocyte-associated antigen 8 precursor 8 - precursor - mouse
N;Alternate names: immediate-early protein 2 (ORF13) homolog
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 26-Aug-1999
C;Accession: I49623
R;Rouvier, E.; Luciani, M.
J. Immunol. 150, 5445-5456, 1993
A;Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instability
A;Reference number: 149623; MUID:93294300
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-150 <RES>
A;Cross references: GB:L13839; NID:g293329; PIDN:AAA37490.1; PID:9293330
C;Genetics:
A;Gene: CtlA-8
C;Superfamily: saimiri herpesvirus immediate-early protein 2

Query Match 14.8% Score 108; DB 2; Length 150;
Best Local Similarity 34.4%; Pred. No. 0.0044;
Matches 31; Conservative 11; Mismatches 42; Indels 6; Gaps 4;

QY 14 RPFTNL RSVSPWAXRISDPARYPRLYPEAVCLCRGCLTGLFGEEDDVFRSAPVYMPVTL 72
DB 57 RSDYLNRTSPWTLSRNEDPVPYSVTEACRHQRVCNA EGKLDHHMMSVLIQEIL 115

QY 73 VIRRTP-ACAGRSVTEAYVTPVGTCV 101
DB 116 VLKREPKCP--FTFRVEKMLVGVGCrCV 142

RESULT 4
T21334
hypothetical protein F25D1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Kelly, P.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19408
A;Accession: T21334
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-148 <WIL>
A;Cross references: ENB:Z733973; PIDN:CAA58268.1; GSPDB:GN00023; CESP:F25D1.3
A;Experimental source: Clone F25D1
C;Genetics:
A;Gene: CESP:F25D1.3
A;Map position: 5
A;Introns: 60/2

Query Match 13.6%; Score 99; DB 2; Length 148;
Best Local Similarity 29.8%; Pred. No. 0.0038;
Matches 28; Conservative 17; Mismatches 35; Indels 14; Gaps 5;

QY 20 RSVSPWAXRISDPARYPRLYPEAYCLCRGCLTGLFGEEDDVFRSAPVYMPVTLRRT 77
DB 52 RALCPWDSSRVNQESREPLTAESVCLRKSGSTGAF-----CPIVKVPLLRV 103

QY 78 PAC--AGGRSVTEAYVTPVG-CTCVPEPERDA 108
DB 104 -SCDRSTGLWNTVRSLTEITVGSCHSVLPRTQRAA 136

RESULT 5
T27843
hypothetical protein ZK39.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Kershaw, J.
submitted to the EMBL Data Library, November 1996
A;Reference number: T27843
A;Accession: T27843
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-226 <WIL>
A;Cross references: ENB:Z82093; PIDN:CA805021.1; GSPDB:GN00019; CESP:ZK39.8
A;Experimental source: Clone ZK39
C;Genetics:
A;Gene: CESP:ZK39.8
A;Map position: 1
A;Introns: 32/1; 52/3; 108/1

Query Match 10.8%; Score 78.5; DB 2; Length 226;
Best Local Similarity 25.4%; Pred. No. 0.85;
Matches 31; Conservative 18; Mismatches 32; Indels 41; Gaps 8;

QY 2 CPAGGRPADRRRPPTNLRSVSPWAXRISDPARYPRLYPEAVCLCRGCLTGLFGEEDDV 60
DB 55 CDAGW---TRRNRP-----GGWCVRF-----LRRTPACAGRSVTEAYVTPVGCTVCEPEKDADSI 103
QY 61 RFRSAPVYMPVY-----LRRTPACAGRSVTEAYVTPVGCTVCEPEKDADSI 111
DB 104 K-KIASLLPQISQQSGSIYIGHRTPACSKS-----PISSC-----NSM 143

QY 112 NS 113
DB 144 NS 145

RESULT 6
B61719
conserved hypothetical protein TC0284 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

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Query Match 24.2%; Score 176.5; DB 5; Length 408;
Best Local Similarity 40.2%; Pred. No. 7.2e-10;
Matches 41; Conservative 9; Mismatches 39; Indels 13; Gaps 2;
;

Qy 17 TNLRSVSPRAYISYDPARYPVLPEAVCLRCGLTGFGEEDVFRSAPVYMPVVLLR 76
Db 93 SNKSLSPGYSINHDPSPILPVDPARCLCGLCVNPFTMOEGRSMYSPVFSQVYVRR 152

Qy 77 -TPACAGGRSVTYTEAYTRIPVGTCV-----PEPE 105
Db 153 LCPPPRTGPQRARVMEIAVGCCTCIFPDKTHTCPPCPAPE 194

RESULT 15
US-09-886-4-04-7
; Sequence 7, Application US/09886404
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIORITY NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-4-04-7

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Query Match 23.9%; Score 174; DB 5; Length 117;
Best Local Similarity 43.7%; Pred. No. 3.3e-10;
Matches 38; Conservative 9; Mismatches 38; Indels 2; Gaps 1;
;

Qy 17 TNLRSVSPRAYISYDPARYPVLPEAVCLRCGLTGFGEEDVFRSAPVYMPVVLLR 76
Db 30 SNKSLSPGYSINHDPSPILPVDPARCLCGLCVNPFTMOEGRSMYSPVFSQVYVRR 89

Qy 77 -TPACAGGRSVTYTEAYTRIPVGTCV 101
Db 90 LCPPPRTGPQRARVMEIAVGCCTCI 116

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Search completed: October 5, 2001, 15:21:23
Job time: 93 sec

; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US00/23522
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/34956
 ; PRIOR FILING DATE: 2000-12-0
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800
 ; PRIOR FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21066
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 80
 ; SEQ ID NO: 11
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-931-836-11

Query Match 25.7%; Score 187.5; DB 5; Length 197;
 Best Local Similarity 40.2%; Pred. No. 2.6e-11; Indels 7; Gaps 1;
 Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

Qy 17 TNLRSVPWARYSPDARYPRVLPAYCCLRGCLTGLFGEEDVFRSAPYMPYTVLRR 6
 Db 101 THQRSTISPVWRYRVDTDERYPQKLAFAECLGCGCIDARTGRRTAALNSVRLQLSLLVRR 160

Qy 77 TPACAGGRSVYTEA-----YVTIPVGCTCY 101
 Db 161 RPCSRDGSGLPLPGAFAHFTEFIHVPVGCTCY 192

RESULT 12
 US-60-309-936-2
 ; Sequence 2, Application US/60309936
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Ling
 ; TITLE OF INVENTION: Methods of Using A Human IL-17 Related Polypeptide To Treat Disease
 ; FILE REFERENCE: P-14089A
 ; CURRENT APPLICATION NUMBER: US/60/309,936
 ; CURRENT FILING DATE: 2001-08-03
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-309-936-2

Query Match 25.7%; Score 187.5; DB 6; Length 197;
 Best Local Similarity 40.2%; Pred. No. 2.6e-11; Indels 7; Gaps 1;
 Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

Qy 17 TNLRSVPWARYSPDARYPRVLPAYCCLRGCLTGLFGEEDVFRSAPYMPYTVLRR 76
 Db 101 THQRSTISPVWRYRVDTDERYPQKLAFAECLGCGCIDARTGRRTAALNSVRLQLSLLVRR 160

Qy 77 TPACAGGRSVYTEA-----YVTIPVGCTCY 101
 Db 161 RPCSRDGSGLPLPGAFAHFTEFIHVPVGCTCY 192

RESULT 13
 US-09-854-280-24
 ; Sequence 24, Application US/09854280
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381RIC2
 ; CURRENT APPLICATION NUMBER: US/09/854,280
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/085,579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: US 60/113,621
 ; PRIOR FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO: 24
 ; LENGTH: 206
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: IL-17C-His tag
 US-09-854-280-24

Query Match 25.7%; Score 187.5; DB 5; Length 206;
 Best Local Similarity 40.2%; Pred. No. 2.8e-11; Indels 7; Gaps 1;
 Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

Qy 17 TNLRSVPWARYSPDARYPRVLPAYCCLRGCLTGLFGEEDVFRSAPYMPYTVLRR 76
 Db 101 THQRSTISPVWRYRVDTDERYPQKLAFAECLGCGCIDARTGRRTAALNSVRLQLSLLVRR 160

Qy 77 TPACAGGRSVYTEA-----YVTIPVGCTCY 101
 Db 161 RPCSRDGSGLPLPGAFAHFTEFIHVPVGCTCY 192

RESULT 14
 US-09-854-280-12
 ; Sequence 12, Application US/09854280
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381RIC2
 ; CURRENT APPLICATION NUMBER: US/09/854,280
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/085,579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: US 60/113,621
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO: 12
 ; LENGTH: 408
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: IL17B-Fc fusion
 US-09-854-280-12

; PRIOR APPLICATION NUMBER: PCT/US99/31274
 ; PRIOR FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/05601
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: PCT/US00/07532
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/30873
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: PCT/US00/34956
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 39
 ; SEQ ID NO: 4
 ; LENGTH: 197
 ; TYPE: PCT
 ; ORGANISM: Homo Sapien
 ; US-09-908-827-4

Query Match 25.7%; Score 187.5; DB 5; Length 197;
 Best Local Similarity 40.2%; Pred. No. 2.6e-11; Gaps 1;
 Matches 37; Conservative 11; Mismatches 37; Indels 7;

Qy	17	TNLRSPWARYSVDARYDRYLPEAYRGCGLTGLFSEEDYERSAVYMPITVLLR	76
Db	101	TIQRTSPWRVRVDTDERYQPKLAFAECLRGCIDARTGRETAAINSVRLQLSLVLR	160
Qy	77	TPACAGGRSYVTEA-----YVTIPVGCRV 101	
Db	161	RPCSRSQSGLPTPGFAFAHTEFIHVPVGCTCV 192	

RESULT 11
 US-09-931-836-11
 ; Sequence 11, Application US/09931836
 ; GENERAL INFORMATION:
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Watanaabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3030R1C1
 ; CURRENT APPLICATION NUMBER: US/09/931,836
 ; CURRENT FILING DATE: 2001-08-16
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/112514
 ; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: 60/1133300
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/113430
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113605
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113621
 ; PRIOR FILING DATE: 2000-03-02

RESULT 8
US-09-480-297A-23
; Sequence 23, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Baran, J. Fernando
; APPLICANT: Kastelain, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO: 23
; SOFTWARE: PatentIn version 3.1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-297A-23

Query Match 25.7%; Score 187.5; DB 5; Length 197;
Best Local Similarity 40.2%; Pred. No. 2.6e-11; Indels 7; Gaps 1;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

QY 17 TNLRSVPWARYSDPARYPRLPEAYCLCRGCLTGLFGEEDVFRSAPVYMPYTVLRR 6
DB 101 THORSISPRYRVDDEDRYPLAKFAECLCRSCIDARTGRETAAALNSVRLLQSLIVLRR 160

QY 77 TPACAGGSVYEA-----YVTIPVGCTV 101
DB 161 RPCSRDGSGLPTPGAFAHTEFHYPVGCTV 192

RESULT 9
US-09-854-280-3
; Sequence 3, Application US/0954280
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLooveren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Williams, P. Mickey
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381RIC1(US)
; CURRENT APPLICATION NUMBER: US/09/908,827
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/1085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/2113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134,287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138,387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14

Query Match 25.7%; Score 187.5; DB 5; Length 197;
Best Local Similarity 40.2%; Pred. No. 2.6e-11; Indels 7; Gaps 1;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

QY 17 TNLRSVPWARYSDPARYPRLPEAYCLCRGCLTGLFGEEDVFRSAPVYMPYTVLRR 6
DB 101 THORSISPRYRVDDEDRYPLAKFAECLCRSCIDARTGRETAAALNSVRLLQSLIVLRR 160

; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: D0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 12
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-480-297A-12

Query Match 82.4%; Score 601; DB 5; Length 205;
Best Local Similarity 83.3%; Pred. No. 1.8e-52;
Matches 110; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 1 SCPGGRPADRFRPPTNLRSVPWARYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
Db 77 SCPGGRADFRFRPPTNLRSVPWARYDPARYPRYLPEAYCLCRGCLTGLFGEEDV 136
Qy 61 RFRSAPVYMPTVLRLTPACAGGRSVTYEAYTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 137 RFRSPVFSPPAVLRLTAAAGGRSVYAHYTIPVGCTCVPCEPDKSADSANSSMD--- 192
Qy 121 KLLGPNDAPAG 132
Db 193 KLLGPADPAG 204

RESULT 5

US-09-480-297A-10

; Sequence 10, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastlein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: D0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-480-297A-10

Query Match 28.5%; Score 208; DB 5; Length 44;
Best Local Similarity 84.1%; Pred. No. 4.6e-14;
Matches 37; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 36 YPRVLPPEAYCLCRGCLTGLFGEEDVFRERSAPVYMPTVLRLRTPA 79
Db 1 FPRVLPPEAYCLCRGCLTGLFGEEDVFRERSAPVESPVVLRLRTAA 44

RESULT 6

US-09-854-280-13

; Sequence 13, Application US/09854280
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P138R1C2
; CURRENT APPLICATION NUMBER: US/09/554,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO: 13
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-17C-FC fusion
; US-09-854-280-13

Query Match 26.5%; Score 193; DB 5; Length 425;
Best Local Similarity 36.4%; Pred. No. 1.7e-11;
Matches 43; Conservative 15; Mismatches 52; Indels 8; Gaps 2;

Qy 17 TNLRSPWARYDPARYPRYLPEAYCLCRGCLTGLFGEEDVFRSAPVYMPTVLRL 76
Db 101 THQRISPRYRVDDEYPQKLAFAEFLCRGCDARTGRETAAALNSVRLLOSSLLVRR 160

Qy 77 TPACAGGRSVYTEA-----YVTIPVGCTVPEPEKDADSINSSIDKQAKLLGPN 127
Db 161 RPCSRDGSGLPPTGAFATHETFHVPVGCTV-LPRTSPVDKTHICPPCPAPELLGGPS 217

RESULT 7
US-09-886-404-8

; Sequence 8, Application US/09886404
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Veh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/386,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/910,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; NUMBER OF SEQ ID NOS: 22
; PRIOR FILING DATE: 2000-06-22
; SEQ ID NO: 8
; LENGTH: 197
; TYPE: PRT
; SOFTWARE: PatentIn Ver. 2.0
; US-09-886-404-8

Query Match 25.7%; Score 187.5; DB 5; Length 197;
Best Local Similarity 40.2%; Pred. No. 2.6e-11;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

Qy 17 TNLRSPWARYDPARYPRYLPEAYCLCRGCLTGLFGEEDVFRSAPVYMPTVLRL 76
Db 101 THQRISPRYRVDDEYPQKLAFAEFLCRGCDARTGRETAAALNSVRLLOSSLLVRR 160

Qy 77 TPACAGGRSVYTEA-----YVTIPVGCTV 101
Db 161 RPCSRDGSGLPPTGAFATHETFHVPVGCTV 192

; APPLICANT: Li, Hanzhong
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: VanLooyen, Menno
 ; APPLICANT: Vandlen, Richard
 ; APPLICANT: Watanabe, Collin
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William
 ; APPLICANT: Yansura, Daniel
 FILE REFERENCE: P1381RICP1C1(US)
 CURRENT APPLICATION NUMBER: US/09/908, 827
 CURRENT FILING DATE: 2001-07-18
 PRIOR APPLICATION NUMBER: 60/085, 579
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/113, 621
 PRIOR FILING DATE: 1998-12-23
 PRIOR APPLICATION NUMBER: 60/130, 232
 PRIOR FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: 60/131, 022
 PRIOR FILING DATE: 1999-04-26
 PRIOR APPLICATION NUMBER: 60/134, 287
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 60/138, 387
 PRIOR FILING DATE: 1999-06-09
 PRIOR APPLICATION NUMBER: 60/172, 096
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/175, 481
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: 60/191, 007
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/213, 807
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 60/242, 837
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: 60/244, 072
 PRIOR FILING DATE: 2000-10-26
 PRIOR APPLICATION NUMBER: 09/311, 832
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 09/380, 138
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/380, 142
 PRIOR FILING DATE: 1999-08-25
 PRIOR APPLICATION NUMBER: 09/644, 848
 PRIOR FILING DATE: 2000-08-22
 PRIOR APPLICATION NUMBER: 09/747, 259
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: 09/816, 744
 PRIOR FILING DATE: 2001-03-22
 PRIOR APPLICATION NUMBER: 09/854, 208
 PRIOR FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: 09/854, 280
 PRIOR FILING DATE: 2001-05-10
 PRIOR APPLICATION NUMBER: PCT/US99/05028
 PRIOR FILING DATE: 1999-03-08
 PRIOR APPLICATION NUMBER: PCT/US99/10733
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: PCT/US99/31244
 PRIOR FILING DATE: 1999-12-30
 PRIOR APPLICATION NUMBER: PCT/US00/04341
 PRIOR FILING DATE: 2000-02-18
 PRIOR APPLICATION NUMBER: PCT/US00/05601
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR APPLICATION NUMBER: PCT/US00/07532
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: PCT/US00/15254
 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: PCT/US00/23338
 PRIOR APPLICATION NUMBER: PCT/US00/30873
 PRIOR FILING DATE: 2000-11-10

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; SEQ ID NO: 8
 ; LENGTH: 202
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-908-827-8

Query Match *99.5%; Score 725; DB 5; Length 202;
 Best Local Similarity 99.2%; Pred. No. 7.8e-65;
 Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPTNLRSVPWARYSPDARYSPVYPLPEAYCLRCGCLTGLRGEDV 60
 Db 70 SCPAGGRPADRRFRPTNLRSVPWARYSPDARYSPVYPLPEAYCLRCGCLTGLRGEDV 129

Qy 61 RFRSAPVYMPTVLRRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSNSIDKQGA 120
 Db 130 RFRSAPVYMPTVLRRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSNSIDKQGA 189

Qy 121 KLLLGPNDAAPGP 133
 Db 190 KLLLGPNDAAPGP 202

RESULT 3
 US-09-480-297A-6

; Sequence 6, Application US/09480297A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
 ; FILE REFERENCE: DIA917K
 ; CURRENT APPLICATION NUMBER: US/09/480, 297A
 ; CURRENT FILING DATE: 2000-01-10
 ; PRIOR APPLICATION NUMBER: 60/115, 506
 ; PRIOR FILING DATE: 1999-01-11
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-480-297A-6

Query Match 84.1%; Score 613; DB 5; Length 151;
 Best Local Similarity 99.1%; Pred. No. 8.1e-52;
 Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPTNLRSVPWARYSPDARYSPVYPLPEAYCLRCGCLTGLRGEDV 60
 Db 40 SCPAGGRPADRRFRPTNLRSVPWARYSPDARYSPVYPLPEAYCLRCGCLTGLRGEDV 99

Qy 61 RFRSAPVYMPTVLRRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSIN 112
 Db 100 RFRSAPVYMPTVLRRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSIN 151

RESULT 4
 US-09-480-297A-12

; Sequence 12, Application US/09480297A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.

Result No.	Score	Query	Match	Length	DB ID	Description
1	729	100.0	202	5	US-09-480-297A-8	Sequence 8, Appli
2	725	99.5	202	5	US-09-480-297A-8	Sequence 8, Appli
3	613	84.1	151	5	US-09-480-297A-6	Sequence 6, Appli
4	601	82.4	205	5	US-09-480-297A-12	Sequence 12, Appli
5	208	28.5	44	5	US-09-480-297A-10	Sequence 10, Appli
6	193	26.5	425	5	US-09-854-280-13	Sequence 13, Appli
7	187.5	25.7	197	5	US-09-886-404-8	Sequence 8, Appli
8	187.5	25.7	197	5	US-09-480-297A-23	Sequence 23, Appli
9	187.5	25.7	197	5	US-09-854-280-3	Sequence 3, Appli
10	187.5	25.7	197	5	US-09-908-827-4	Sequence 4, Appli
11	187.5	25.7	197	5	US-09-931-336-11	Sequence 11, Appli
12	187.5	25.7	197	6	US-60-309-936-2	Sequence 2, Appli
13	187.5	25.7	206	5	US-09-854-280-24	Sequence 24, Appli
14	176.5	24.2	408	5	US-09-854-280-12	Sequence 12, Appli
15	174	23.9	117	5	US-09-886-404-7	Sequence 7, Appli
16	174	23.9	175	5	US-09-854-280-23	Sequence 23, Appli
17	174	23.9	180	5	US-09-480-297A-2	Sequence 2, Appli
18	174	23.9	180	5	US-09-854-280-1	Sequence 1, Appli
19	174	23.9	180	5	US-09-908-827-2	Sequence 2, Appli
20	174	23.9	180	5	US-09-929-404-150	Sequence 150, Appli
21	173	23.7	180	5	US-09-480-297A-4	Sequence 4, Appli
22	169	23.2	117	5	US-09-886-404-6	Sequence 6, Appli
23	155.5	21.3	163	5	US-09-908-827-10	Sequence 10, Appli
24	139.5	19.1	123	5	US-09-297A-21	Sequence 21, Appli
25	130.5	17.9	155	5	US-09-886-404-5	Sequence 5, Appli
26	130.5	17.9	155	5	US-09-480-297A-33	Sequence 33, Appli
27	130.5	17.9	155	5	US-09-854-280-11	Sequence 11, Appli

LENGTH: 186
 ;
 TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-154-817-4

Query Match 100.0%; Score 729; DB 15; Length 186;
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 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCAGGGRPADRFRPPTNLSRSPWARYSDARYPRYLPPAYCLRGCLTGLFGEDEV 60
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Qy 61 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 120
 Db 114 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 173

Qy 121 KLLGPNDAPGP 133
 Db 174 KLLGPNDAPGP 186

RESULT 13
US-09-397-816-4

; Sequence 4, Application US/09397846
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; ATTORNEY: Taff, David W.
 ; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
 ; CURRENT APPLICATION NUMBER: US/09/397,846
 ; FILE REFERENCE: 98-54
 ; CURRENT FILING DATE: 1999-09-17
 ; EARLIER APPLICATION NUMBER: 60/100,706
 ; EARLIER FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-397-816-4

Query Match 100.0%; Score 729; DB 17; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.7e-73;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCAGGGRPADRFRPPTNLSRSPWARYSDARYPRYLPPAYCLRGCLTGLFGEDEV 60
 Db 54 SCAGGGRPADRFRPPTNLSRSPWARYSDARYPRYLPPAYCLRGCLTGLFGEDEV 113

Qy 61 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 120
 Db 114 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 173

Qy 121 KLLGPNDAPGP 133
 Db 174 KLLGPNDAPGP 186

RESULT 14
US-09-397-816B-4

; Sequence 4, Application US/09397846B
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; ATTORNEY: Taff, David W.
 ; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
 ; CURRENT APPLICATION NUMBER: 98-54
 ; FILE REFERENCE: 98-54
 ; CURRENT FILING DATE: 1998-09-17
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-154-817-3

Query Match 100.0%; Score 729; DB 15; Length 187;
 Best Local Similarity 100.0%; Pred. No. 1.7e-73;
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCAGGGRPADRFRPPTNLSRSPWARYSDARYPRYLPPAYCLRGCLTGLFGEDEV 60
 Db 54 SCAGGGRPADRFRPPTNLSRSPWARYSDARYPRYLPPAYCLRGCLTGLFGEDEV 113

Qy 61 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 120
 Db 114 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 173

Qy 61 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 120
 Db 115 RFRSAPYMPVTYLLRTPACAGGRSVYTEAYTTIPVGCTCYPEPEKDADSINNSIDKQGA 174

Qy 121 KLLGPNDAPGP 133
 Db 175 KLLGPNDAPGP 187

Search completed: October 5, 2001, 15:22:57
Job time: 187 sec

Query Match 100.0%; Score 729; DB 21; Length 173;
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 Matches 133; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
 Db 41 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 100

Qy 61 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 120
 Db 101 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 160

Qy 121 KLLIGPNDAPGP 133
 Db 161 KLLIGPNDAPGP 173

RESULT 9
 US-09-154-817-5
 ; Sequence 5, Application US/09154817
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott
 ; ATTORNEY: Taft, David W.
 ; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
 ; CURRENT APPLICATION NUMBER: US/09/154,817
 ; CURRENT FILING DATE: 1998-09-17
 ; SEQ ID NO: 7
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-154-817-5

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 Best Local Similarity 100.0%; Pred. No. 1.7e-73;
 Matches 133; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
 Db 53 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 112

Qy 61 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 120
 Db 113 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 172

Qy 121 KLLIGPNDAPGP 133
 Db 173 KLLIGPNDAPGP 185

RESULT 10
 US-09-397-846-5
 ; Sequence 5, Application US/09397846
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott
 ; ATTORNEY: Taft, David W.
 ; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
 ; CURRENT APPLICATION NUMBER: US/09/397,846
 ; CURRENT FILING DATE: 1998-09-17
 ; SEQ ID NO: 5
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-397-846-5

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 Best Local Similarity 100.0%; Pred. No. 1.7e-73;
 Matches 133; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
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Qy 61 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 120
 Db 113 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 172

Qy 121 KLLIGPNDAPGP 133
 Db 173 KLLIGPNDAPGP 185

RESULT 12
 US-09-154-817-4
 ; Sequence 4, Application US/09154817
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott
 ; ATTORNEY: Taft, David W.
 ; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
 ; CURRENT APPLICATION NUMBER: US/09/154,817
 ; CURRENT FILING DATE: 1998-09-17
 ; SEQ ID NO: 5
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-154-817-4

Query Match 100.0%; Score 729; DB 17; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.7e-73;
 Matches 133; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 60
 Db 53 SCPAGGRPADRRFRPPTNLRSVSPWARYSDPARYPRYLPEAYCLCRGCLTGLFGEEDV 112

Qy 61 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 120
 Db 113 RFRSAPVYMPVTVLRTPACAGGRSVYTEAVTIPVGCTCYPEPEKDADSINSIDKQGA 172

Qy 121 KLLIGPNDAPGP 133
 Db 173 KLLIGPNDAPGP 185

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; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-4

Query Match 100.0%; Score 729; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SCPAGGRPADRFRPPNLRSPWARYSPDARYPRYLPPAYCLRGCLTGLFGEDEV 60
Db 28 SCPAGGRPADRFRPPNLRSPWARYSPDARYPRYLPPAYCLRGCLTGLFGEDEV 87
Qy 61 RFRSAPVYMPVTYLLRTPACAGGRSYTYEAVTIPVGCTCYVEPEKADSINSSIDQGA 120
Db 88 RFRSAPVYMPVTYLLRTPACAGGRSYTYEAVTIPVGCTCYVEPEKADSINSSIDQGA 147
Qy 121 KLLGPNDAPGP 133
Db 148 KLLGPNDAPGP 160

RESULT 6
PCT-US99-11644-32
; Sequence 32, Application PC/TUS9911644
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PFA4/OPCT
; CURRENT APPLICATION NUMBER: PCT/US99/11644
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-11644-32

Query Match 100.0%; Score 729; DB 1; Length 173;
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Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SCPAGGRPADRFRPPNLRSPWARYSPDARYPRYLPPAYCLRGCLTGLFGEDEV 60
Db 41 SCPAGGRPADRFRPPNLRSPWARYSPDARYPRYLPPAYCLRGCLTGLFGEDEV 100
Qy 61 RFRSAPVYMPVTYLLRTPACAGGRSYTYEAVTIPVGCTCYPEPEKDADSINSSIDQGA 120
Db 101 RFRSAPVYMPVTYLLRTPACAGGRSYTYEAVTIPVGCTCYPEPEKDADSINSSIDQGA 160

RESULT 8
US-09-731-816-32
; Sequence 32, Application US/09731816
; GENERAL INFORMATION:
; APPLICANT: Ender, Reinhard
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PFA4/OPCT
; CURRENT APPLICATION NUMBER: US/09731816
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-32

Query Match 100.0%; Score 729; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SCPAGGRPADRFRPPNLRSPWARYSPDARYPRYLPPAYCLRGCLTGLFGEDEV 60
Db 41 SCPAGGRPADRFRPPNLRSPWARYSPDARYPRYLPPAYCLRGCLTGLFGEDEV 100
Qy 61 RFRSAPVYMPVTYLLRTPACAGGRSYTYEAVTIPVGCTCYPEPEKDADSINSSIDQGA 120
Db 101 RFRSAPVYMPVTYLLRTPACAGGRSYTYEAVTIPVGCTCYPEPEKDADSINSSIDQGA 160
Qy 121 KLLGPNDAPGP 133
Db 161 KLLGPNDAPGP 173

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RESULT 2
 PCT-US99-11644-4
; Sequence 4, Application PC/TUS9911644
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PCT/0PCT
; CURRENT APPLICATION NUMBER: PCT/TUS99/11644
; EARLIER APPLICATION NUMBER: 60/087, 3440
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/089, 805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131, 965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
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; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
 PCT-US99-11644-4

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 Db 28 SCPAGGRPADRFRPTNLRSVSPWARYRISDAPRYLPAYCLCRGCLTGLFGEDEVY 87

Qy 61 RFRSAPYMPVVLRRTPACAGRSYTYEAVTIPVGCTVPEPEKDADSINSSIDKQGA 120
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Qy 121 KLLLGPNDAAGP 133
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RESULT 3
 US-09-231-748-12
; Sequence 12, Application US/09231788A
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: P399P1
; CURRENT APPLICATION NUMBER: US/09/231,788A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: 60/052, 870
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
 US-09-231-748-12

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 Db 88 RFRSAPYMPVVLRRTPACAGRSYTYEAVTIPVGCTVPEPEKDADSINSSIDKQGA 147

Qy 121 KLLLGPNDAAGP 133
 Db 148 KLLLGPNDAAGP 160

RESULT 5
 US-09-731-816-4
; Sequence 4, Application US/09731816
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: P470P1
; CURRENT APPLICATION NUMBER: US/09/731,816
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169, 837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US/09/320, 713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087, 340
; PRIOR FILING DATE: 1998-05-29

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Om protein - protein search, using sw model.

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Sequence 4, Appli
Sequence 8, Appli

ALIGNMENTS

RESULT 1
PCT-US00-00807-12
; Sequence 12, Application PC/TUS0000807
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399PC12
; CURRENT APPLICATION NUMBER: PCT/US00/00807
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: 09/231,788
; EARLIER FILING DATE: 1998-01-15
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO: 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-00807-12

Query Match 100.0%; Score 729; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCPAGGRPADRRFRPTNLRSPWARYSDPARYPRYLPEAYCLCRLGCLTGLFGEVDY 60
Db 28 SCPAGGRPADRRFRPTNLRSPWARYSDPARYPRYLPEAYCLCRLGCLTGLFGEVDY 87
Qy 61 RFRSAPVMPMTVLLRRTACAGGRSRVTEAYVTPVGCTCVPEPEKDADSINSIDKGKA 120
Db 88 RFRSAPVMPMTVLLRRTACAGGRSRVTEAYVTPVGCTCVPEPEKDADSINSIDKGKA 147
Qy 121 KLLGPNDAPGP 133

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4	729	100.0	160 17	US-09-320-713-4	Sequence 4, Appli	
5	729	100.0	160 21	US-09-731-816-4	Sequence 32, Appli	
6	729	100.0	173 1	PCT-US99-11644-32	Sequence 32, Appli	
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8	729	100.0	173 21	US-09-731-816-32	Sequence 32, Appli	
9	729	100.0	185 15	US-09-154-817-5	Sequence 5, Appli	
10	729	100.0	185 17	US-09-397-846-5	Sequence 5, Appli	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

; TELEPHONE: (206)587-0430
; TELEFAX: (206)
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; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-696-8

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Db	121	-- -GHQPCPNSFRERMLVTVGCTCY	143

Search completed: October 5, 2001, 15:20:11
Job time: 21 sec

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentnet Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/034,810
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/685,239
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: GI5262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 151 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-034-810-6

Query Match 14.9%; Score 108.5; DB 3; Length 151;
 Best Local Similarity 31.4%; Pred. No. 3.3e-05;
 Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

Qy 20 RSVSPWAVRISYDPARYPRLPEAYCLCRGCLTGGLFGEEDVFRSAPYMPTVYLRRTPA 79
 Db 65 RSTSPWTLARNEDODRPSVIAWEAKCRYLGCVNA-DGNYDYHMSNSVP1QEELVVRK -- 120

Qy 80 CAGGRSVTEAY---VTIPVGCTCV 101
 Db 121 --GHQPCPNFSRLEKMLTVGCTCV 143

RESULT 14
 US-09-022-255-8
 Sequence 8, Application US/09022255
 Patent No. 6072033
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,255
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,694
 FILING DATE: 21 MARCH 1996
 APPLICATION NUMBER: USN 08/538,765
 FILING DATE: 7 AUGUST 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 08/410,535
 FILING DATE: 23 MARCH 1995
 ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 151 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Herpesvirus Saimiri
 SPRAIN: ORF13
 US-09-022-255-8

Query Match 14.9%; Score 108.5; DB 3; Length 151;
 Best Local Similarity 31.4%; Pred. No. 3.3e-05;
 Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

Qy 20 RSVSPWAVRISYDPARYPRLPEAYCLCRGCLTGGLFGEEDVFRSAPYMPTVYLRRTPA 79
 Db 65 RSTSPWTLARNEDODRPSVIAWEAKCRYLGCVNA-DGNYDYHMSNSVP1QEELVVRK -- 120

Qy 80 CAGGRSVTEAY---VTIPVGCTCV 101
 Db 121 --GHQPCPNFSRLEKMLTVGCTCV 143

RESULT 15
 US-09-022-696-8
 Sequence 8, Application US/09022696
 Patent No. 6072037
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 APPLICANT: Spriggs, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,696
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE: 23 MARCH 1995
 APPLICATION NUMBER: USN 08/410,535
 FILING DATE: 21 MARCH 1996
 APPLICATION NUMBER: USN 08/538,765
 FILING DATE: 7 AUGUST 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USN 08/410,535
 FILING DATE: 23 MARCH 1995
 ATTORNEY/AGENT INFORMATION:

STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,257
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/410,535
 FILING DATE: 23 MARCH 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REFERENCE/DOCKET NUMBER: 34-695
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 158 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Herpesvirus Saimiri
 STRAIN: ORF13
 US-08-620-694A-8

Query Match 15.4%; Score 112; DB 4; Length 158;
 Best Local Similarity 33.3%; Pred. No. 1.4e-05;
 Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

Qy 5 GERPADRRFRPPINL-RSVPSPAYRISDPAVYCLRGCLTGLEEDYFR 63
 Db 58 GAKYSSR-RPSDYLNRNSTSPWLHRSNEDPDYPSVIAQCRHORCVNA-EGKLDDHHMN 114

Query Match 14.9%; Score 108.5; DB 2; Length 151;
 Best Local Similarity 31.4%; Pred. No. 3.3e-05;
 Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

Qy 20 RSYSPWAXRISDPAVRYPLPEAYCLRGCLTGLEEDYFRSAVYMPTVLRLRTPA 79
 Db 65 RSTSPWTLHRSNEQDRYPSVIAEKRCRYLGCYNA-DGNVDYHMNSVPIQQETLVVRK-- 120

Query Match 14.9%; Score 108.5; DB 2; Length 151;
 Best Local Similarity 31.4%; Pred. No. 3.3e-05;
 Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

Qy 80 CAGRSVTEAY---VTPVGCTC 101
 Db 121 --GHQPPNSFRLEKMLVTVGCTC 143

RESULT 13
 US-09-034-810-6
 Sequence 6, Application US/09/034810
 Patent No. 6043344

GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: Kelleher, Kerry
 APPLICANT: Carlin, McKeough
 APPLICANT: Goldman, Samuel
 APPLICANT: Pittman, Debra
 APPLICANT: Mi, Sha
 APPLICANT: Neben, Steven
 APPLICANT: Giannotti, JoAnn
 APPLICANT: Golden Fleet, Margaret
 TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins
 NUMBER OF SEQUENCES: 9
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1

Db	58	GAKVSSR - RPSDYNLRNSTPWTLLRNEDDRYPSIVWEAQRHORCVNA - EGKLDHMMN	114
Qy	64	SAPVMPYTVLRRTP - ACAGGRSVTYEAVVTTIPGCTV	101
Db	115	SVLQEELIYLKREPECL - FEVERMLVGGCTV	150

Sequence 7, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, William
APPLICANT: Farnsworth, William

RESULT 9
•09-022-260-7
Sequence 7, Application US/09022260

ENT No. 6100235
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6100235el Receptor That Binds IB-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/0022,260
FILING DATE: 08/09/2002,260

CLASSIFICATION:
APPLICATION NUMBER: 08/620,694
FILING DATE: 23 MARCH 1995

CLASSIFICATION:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
MOL-09-0022,260-7

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; Sequence 7, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Springs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: NO. 6191104e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/0022,259
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-0022-259-7

; Query Match 15 4% Score 112; DB 4; Length 158;
; Best Local Similarity 33.3%; Pred. No. 1.4e-05;
; Matches 33; Conservative 14; Mismatches 44; Indels 8
; GGRPADRRFRPPTNL-RSVPSPWAVRISYDPARYPLPEAYCLCRGCLTGEGEE
; 5 GAKVSSR-RPSDYLNRNSTSPWTLHRRNEDPDRYPSWIEAQCRHQRCVNA-EGKLL
; 58 Qy 64 SAVPYMPITVLRPTP-ACAGGRSYTEAVTIPVGCTV 101
; 115 SVLIQKEIILVKREPSCP--FTRFRVERKMLVGVGCTV 150
; Db RESULT 11
; US-09-0022-257-7
; Sequence 7, Application US/09022257
; Patent No. 6191525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Springs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: NO. 6197525e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation

```

REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 6072037
 FAX: (206)
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 158 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-022-255-7

Query Match 15.4%; Score 112; DB 3; Length 158;
 Best Local Similarity 33.3%; Pred. No. 1.e-05;
 Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

Qy 5 GGRPADRRRFPPTNL-RSVSPWARYISDPRYPLPEAKYCLRGCLTGLEEDVYFR 63
 Db 58 GAKVSSR-RPSDYLNRTSPNTLHRNEDPDRYSPVIWEAQQRHQCVNA-EGKLDHHM 114

Query Match 15.4%; Score 112; DB 3; Length 158;
 Best Local Similarity 33.3%; Pred. No. 1.e-05;
 Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

RESULT 8
 US-09-022-255-7
 Sequence 7, Application US/09022253
 Patent No. 6096305
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 SPRIGGS, Melanie
 APPLICANT: Fanslow, William
 TITLE OF INVENTION: NC. 6096305el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/022,253
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 FAX: (206) 6072037
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 158 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 15.4%; Score 112; DB 3; Length 158;
 Best Local Similarity 33.3%; Pred. No. 1.e-05;
 Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

Qy 64 SAPVYMPFVVLRLRTP-ACAGGRSVYTEAYVTIPVGCTC 101
 Db 115 SVLIQEQELVLKRPEPSCP--FTFRVEKMLVGVGCTC 150

Query Match 15.4%; Score 112; DB 3; Length 158;
 Best Local Similarity 33.3%; Pred. No. 1.e-05;
 Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

Qy 5 GGRPADRRRFPPTNL-RSVSPWARYISDPRYPLPEAKYCLRGCLTGLEEDVYFR 63

Db 36 SCPPVPGGSMKLDIGLINENQRVMSMRNIESRSTSPPWNYTVWDPNRYPSEVQACRNL 95
 Qy 49 GCLTGFLFGEEDYRERSAPVYMPVVRRTPACAGGSV-YTEAYYTVIYGCTV 101
 Db 96 GCINAQ-GKEDISMNVSPIQQETLVVRRKHQ--GCSVSFOLEKVLTVGCTV 145

RESULT 2
 US-08-833-823-12
 Sequence 12, Application US/088333823
 Patent No. 5963093
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 ADDRESS: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/833,823
 FILING DATE: 10-APR-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/514,014
 FILING DATE: 11-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: GI6000
 TELEPHONE: (617) 498-8244
 TELEX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 153 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-833-823-12

Query Match 21.3%; Score 155.5; DB 3; Length 163;
 Best Local Similarity 36.0%; Pred. No. 1.3e-10;
 Matches 41; Conservative 15; Mismatches 41; Indels 17; Gaps 6;

Qy 1 SC---PAGGRPAD-----RSVSPWARYSDPARYPRLYPEAYCLCR 48
 Db 36 SCPPVPGGSMKLDIGLINENQRVMSMRNIESRSTSPPWNYTVWDPNRYPSEVQACRNL 95
 Qy 49 GCLTGFLFGEEDYRERSAPVYMPVVRRTPACAGGSV-YTEAYYTVIYGCTV 101
 Db 96 GCINAQ-GKEDISMNVSPIQQETLVVRRKHQ--GCSVSFOLEKVLTVGCTV 145

RESULT 3
 US-09-034-810-2
 Sequence 2, Application US/09034810
 Patent No. 604344
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

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APPLICANT: Goldman, Samuel

APPLICANT: Pittman, Debra

APPLICANT: Neben, Steven

APPLICANT: Giannotti, John

APPLICANT: Golden'Fleet, Margaret

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

APPLICANT: Goldman, Samuel

</div

1 protein - protein search, using sw mode

on: October 5, 2001, 15:19:50 ; Search time 12.19 Seconds
 (without alignments)

224.653 Million cell updates/sec

title:	US-08-320-713-4_COPY_28_160
perfect score:	729
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scoring table:	BLOSUM62
gapopen:	Gapext 0.5
searched:	197319 seqs, 20590346 residues
total number of hits satisfying chosen parameters:	197339
minimum DB seq length:	0
maximum DB seq length:	2000000000
post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries

database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMBO.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	155.5	21.3	153	1 US-08-514-014-12	Sequence 12, Appl
2	155.5	21.3	153	2 US-08-823-12	Sequence 12, Appl
3	155.5	21.3	163	3 US-09-034-810-2	Sequence 2, Appl
4	155.5	21.3	163	3 US-08-685-239-2	Sequence 2, Appl
5	112	15.4	158	2 US-08-620-694A-7	Sequence 7, Appl
6	112	15.4	158	3 US-09-022-255-7	Sequence 7, Appl
7	112	15.4	158	3 US-09-022-696-7	Sequence 7, Appl
8	112	15.4	158	3 US-09-022-257-7	Sequence 7, Appl
9	112	15.4	158	3 US-09-022-260-7	Sequence 7, Appl
10	112	15.4	158	4 US-09-022-259-7	Sequence 7, Appl
11	12	108.5	14.9	151	2 US-08-620-694A-8
12	12	108.5	14.9	151	3 US-09-022-260-8
13	108.5	14.9	151	3 US-09-034-810-6	
14	108.5	14.9	151	3 US-09-022-255-8	
15	108.5	14.9	151	3 US-09-022-696-8	
16	108.5	14.9	151	3 US-08-685-239-6	
17	108.5	14.9	151	3 US-09-022-253-8	
18	108.5	14.9	151	3 US-09-022-260-8	
19	108.5	14.9	151	4 US-09-022-259-8	
20	108.5	14.9	151	4 US-09-022-257-8	
21	108	14.8	150	3 US-09-034-810-4	
22	108	14.8	150	3 US-09-022-696-8	
23	75	10.3	361	2 US-08-413-926A-9	
24	72	9.9	397	5 PCT-US94-09700-11	
25	71.5	9.8	164	1 US-07-970-462A-2	
26	71.5	9.8	164	1 US-08-154-915-6	
27	71.5	9.8	164	1 US-08-446-248-2	
28	71.5	9.8	164	1 US-08-574-043A-2	
29	71.5	9.8	164	2 US-08-524-218A-2	
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32	71.5	9.8	164	5 PCT-US94-09700-2	
33	71.5	9.8	164	5 PCT-US94-12936-2	
34	71.5	9.8	120	6 5514582-36	
35	70.5	9.7	120	6 5514582-36	
36	70.5	9.7	164	1 US-08-275-983B-4	
37	69	9.5	362	2 US-08-737-045-13	
38	68	9.3	492	4 US-09-413-814-72	
39	67	9.2	199	4 US-09-188-930-390	
40	66	9.1	299	4 US-09-188-930-392	
41	66	9.1	299	4 US-09-188-930-392	
42	66	9.1	676	1 US-08-343-785-8	
43	66	9.1	676	2 US-08-462-221-2	
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45	66	9.1	676	2 US-08-462-221-2	

RESULT 1
 US-08-514-014-12
 ; Sequence 12, Application US/08514014
 ; Patent No. 570729

; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Carlin, McTeough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; TITLE OF INVENTION: ENCODED THEREBY
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140

; COMPUTER READEABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/514_014
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32_724
 ; FILING NUMBER: GI6000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 877-8551
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 153 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-514-014-12

Query Match 21.3%; Score 155.5; DB 1;
 Best Local Similarity 36.0%; Pred. No. 1.2e-10;
 Matches 41; Conservative 15; Mismatches 41; Indels 17; Gaps 6

Qy 1 SC ---PAGRPAD-----RRFRPTIL---RSVPWYRISDPARYLPAYCJCR 48

CC associated with abnormal physiology or development, including abnormal
CC proliferation, e.g. cancerous conditions, or degenerative conditions.
CC The IL-171 protein can be used in kits and assay methods for identifying
CC compounds that selectively bind to IL-171.

XX Sequence 205 AA;

Query Match	82.4%	Score 601;	DB 21;	Length 205;
Best Local Similarity	83.3%;	Pred. No. 4	5e-01;	
Matches	110;	Conservative	6;	Mismatches 12; Indels 4; Gaps 1;
Qy	1	SCPAGGRPADRFRFRPTNLRSVSPWARYRISYDARYPRYLPEAYCLCRGCLTGLFGEEDV	60	
Db	77	scpagraadrrfrppnrlrsvpwaryrissypwarysdpairprypeayclrcgcgtgycgef	136	
Qy	61	RFRSAPVYMPTRVLRRTPACAGGRSVYTEAYTIPVGCTCYPEPEKDADSTINSSIDKQGA	120	
Db	137	rfrstpfspavvrrtaacaggrsvyaehytipvgctcypepdksadsanssmd----	192	
Qy	121	KLLGPMDAPG	132	
Db	193	kllqpdapq	204	

Search completed: October 5, 2001, 15:20:59
Job time: 69 sec

Pt New DNA sequence encoding a mammalian homolog of CTLA-8, designated Interleukin-171 (IL-171), useful for recombinant production of IL-171 which can be used for treating conditions associated with abnormal physiology or development -
 Px Disclosure; Page 97; 111pp; English.
 XX The present sequence represents an interleukin (IL)-173 polypeptide. It is a mammalian homologue of the cytokine designated cTLA-8 (also referred to as IL-17). The specification also describes homologues IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA sequence encoding IL-171 is useful for identifying genes, mRNA and cDNA molecules which code for related or homologous proteins. The IL-171 protein, antibodies against IL-171, and compounds which have binding affinity to IL-171 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. The IL-171 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-171.
 XX Sequence 151 AA;
 SQ Query Match 84.1%; Score 613; DB 21; Length 151;
 Best Local Similarity 99.1%; Pred. No. 1.4e-61;
 Matches 111; Conservative 0; Indels 0; Gaps 0;
 Qy 1 SCPPAGRPADRFPRPPNRLRSVSPWARYSPDARYPRYLPEAYCICRGCTGLFGEEDV 60
 Db 40 SCPPAGRPADRFPRPPNRLRSVSPWARYSPDARYPRYLPEAYCICRGCTGLFGEEDV 99
 Qy 61 RFRSAPYMPVYLRLTPACAGGRSYTEAVTIPVGCTCPYCEPEKDADSIN 112
 Db 100 RFRSAPYMPVYLRLTPACAGGRSYTEAVTIPVGCTCPYCEPEKDADSIN 151

RESULT 13

AY70658 1
 ID AAY70658 standard; Protein: 183 AA.
 XX AAY70658;

XX 18-JUL-2000 (first entry)

DE Mature murine transforming growth factor beta-9, ztgfbeta-9 protein.
 KW Murine transforming growth factor beta-9; ztgfbeta-9;
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
 KW antiviral; cytostatic.

XX Mus sp.
 XX WO200015798-A2.
 XX 23-MAR-2000.
 PD XX 17-SEP-1999; 99WO-US21677.
 PF XX 17-SEP-1998; 98US-0154817.
 PA (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Taft DW, Foley KP;
 XX WPI: 2000-271436/23.
 DR N-PSDB; AA252198.
 PR Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated ztgf beta-9, useful as an antiviral and antiproliferative agent -
 XX

PS Claim 6; Page 89; 97pp; English.

XX The present sequence is the mature murine transforming growth factor beta-9, designated ztgf beta-9. The signal sequence extends from amino acid residues 1 to 22. Murine ztgf beta-9 was found to be highly expressed in the HCL hypothalamic cell line. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.

SQ Sequence 183 AA;

Query Match 82.4%; Score 601; DB 21; Length 183;
 Best Local Similarity 83.3%; Pred. No. 3.9e-60;
 Matches 110; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 1 SCPPAGRPADRFPRPPNRLRSVSPWARYSPDARYPRYLPEAYCICRGCTGLFGEEDV 60

Db 55 SCPPAGRPADRFPRPPNRLRSVSPWARYSPDARYPRYLPEAYCICRGCTGLFGEEDV 114

Qy 61 RFRSAPYMPVYLRLTPACAGGRSYTEAVTIPVGCTCPYCEPEKDADSINSSIDKOGA 120

Db 115 RFRSAPVYMPVYLRLTPACAGGRSYTEAVTIPVGCTCPYCEPEKDADSINSSIDKOGA --- 170

Qy 121 KLLGPNDAAPAG 132

Db 171 KLLGPNDAAPAG 182

RESULT 14

AAB07597 1
 ID AAB07597 standard; Protein: 205 AA.
 XX AAB07597;

AC XX

DT 07-NOV-2000 (first entry)

DE A murine interleukin (IL) 173 polypeptide.
 XX KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176; IL-177; IL-171; cell proliferation; cancer.

XX OS Mus sp.

XX Key PH Peptide

XX Location/Qualifiers 1..24

FT FT "signal peptide"

FT FT 25..205

FT FT "mature protein"

FT FT 50

FT FT "phosphorylation site"

FT FT 51..53

FT FT "N-glycosylation site"

FT FT 53

FT FT "phosphorylation site"

FT FT 57..61

FT FT "myristoylation site"

FT FT 80

FT FT "phosphorylation site"

FT FT 82

FT FT "phosphorylation site"

FT FT 82..84

FT FT "phosphorylation site"

FT FT 101..105

FT FT "calcium phosphorylation site"

FT FT 113

FT FT "myristoylation site"

FT FT 116

FT FT "phosphorylation site"

FH	Key Peptide	Location/Qualifiers	
FT		1..22	
XX		/label= Signal_peptide	
PN	WO200015798-A2.		
XX			
PD	23 MAR-2000.		
XX			
PF	17-SEP-1999; 99WO-US21677.		
XX			
PR	17-SEP-1998; 98US-0154817.		
XX			
PA	(ZIMO) ZYMOGENETICS INC.		
XX			
PI	Presnell SR, Taft DW, Foley KP;		
XX			
DR	WPI; 2000-271436/23.		
N-PSDB;	AAZ52201.		
XX			
PT	Polynucleotides encoding a novel transforming growth factor beta-9, useful as an antiviral and polypeptide, designated ztgf beta-9, useful as an antiviral and antiproliferative agent -		
PT			
XX			
PS	Claim 6; Page 92-93; 97PP; English.		
XX			
CC	The present sequence is a variant of human transforming growth factor beta-9, designated ztgf beta-9. Human ztgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies or demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.		
CC			
XX			
Sequence	209 AA;		
Query	1 SCPGAGRPADRRPPTNLRSVSPWARYSPDARYSPWARYSPVAYTIPVGCTCYPEPEKDAADSIN 112	Match	84.1%; Score 613; DB 21; Length 151;
Best Local Similarity	100.0%	Best Local Similarity	99.1%; Pred. No. 1..e-61;
Matches	133;	Matches	111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Conservative	0;		
Db	100 rfrsapymptvrlrtpacagrsyvteaytvpgrctvpepekdadsin 151	RESULT	12
Qy	1 SCPGAGRPADRRPPTNLRSVSPWARYSPDARYSPWARYSPVAYTIPVGCTCYPEPEKDAADSIN 112	ID	AAB07690 standard; Protein: 151 AA.
Db	77 scpaggrpadrrtrpptrnlrsvspwarysparyspvaytvpgrctvpepekdadsin 136	XX	
Qy	61 RFRSAPYMPVTVLRLRTPACAGRSYVTEAYTIPVGCTCYPEPEKDADSINSSIDKQGA 120	AC	AAB07690;
Db	137 rfrsapymptvrlrtpacagrsyvteaytvpgrctvpepekdadsinssidkqga 196	XX	
Qy	121 KLLGPNDAPAGP 133	DT	07-NOV-2000 (first entry)
Db	197 kllgpndapagp 209	XX	
OS	Rattus sp.	DE	A rat interleukin-173 polypeptide.
XX		XX	
ID	AAB07594 standard; Protein: 151 AA.	PN	WO20042187-A1.
XX		XX	
AC	AAB07594;	PD	20-JUL-2000.
XX		XX	
DT	07-NOV-2000 (first entry)	PF	10-JAN-2000; 99US-0000005.
XX		XX	
DE	A human interleukin (IL) 173 polypeptide.	PR	11-JAN-1999; 99US-0229402.
XX		XX	
KW	Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176; IL-177; IL-171; cell proliferation; cancer.	PA	(SCHE) SCHERING CORP.
XX		XX	
OS	Homo sapiens.	PI	Gorman DM, Bazan JF, Kastelein RA;
XX		DR	WP; 2000-476060/41.
PN	WO20042188-A2.	DR	N-PSDB; AAA59156.
XX		XX	

Qy	1	SCPAGRPADRRRPFPTNLRSPWARYSPDAPYRPLPEAYCLRCGLTGLEEVD
Db	54	scpagrpadrfrfppthlrspwarysydparypyipeayclrcgtlgfeedy
Qy	61	RFRSAPVYMPVTYLRTPACAGGRSYVTEAYVTIPVGCTCPYPEPKDADSINSSIDKOGA
Db	114	rfrsaaevmpvvirrtpacaggrrsvteayvtipvgctcpypepkdadsinssidkqga
Qy	121	KLLGPNDAPAGP
Db	174	kllqpndapaq

RESULT	5
AAV70654	
ID	AAV70654 standard; protein: 187 AA.
XX	
AC	AAV70654;
XX	
DT	18-JUL-2000 (first entry)
XX	
DE	Mature human transforming growth factor beta-9, ztgbeta-9 protein-1.
XX	
KW	Human transforming growth factor beta-9; ztgf beta-9;
XX	Alzheimer's disease; neurodegenerative disease; Huntington's disease;
KW	amyotrophic lateral sclerosis; ALS; Parkinson's disease;
KW	peripheral neuropathy; demyelinating disease; multiple sclerosis;
KW	antiviral; cytocatic.

XX WO2000015798-A2.
PN XX
PD XX
23-MAR-2000.
XX PF 17-SEP-1999; 99WO-US21677.
XX PR 17-SEP-1998; 98US-0154817.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Presnell SR, Taft DW, Foley KP;
XX DR WPI; 2000-271136/23.
DR NPSDB: AA252195.

polynucleotides encoding a novel transforming growth factor beta-9, useful as an antiviral and
polypeptide, designated Ztgf beta-9, useful as an antiviral and
anti-proliferative agent -

Claim 6; Page 84; 97pp; English.

The present sequence is the mature human transforming growth factor beta-9, designated Ztgf beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 16 to and including amino acid 202 of Ztgf beta-9. Human Ztgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or denervation diseases including multiple sclerosis. Ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.

SQ	Sequence	187 AA;
Query Match	100.0%	Score 729;
Best Local Similarity	100.0%	Pred. No. 1. 4e-74;
Matches 133; Conservative	0;	Mismatches 0;
		Indels 0;
		Gaps 0;
		Length 187;

RESULT 6
AAY70663 ID AAY70663 standard. Protein: 187 AA

AA	AAY70663;	
AC		
XX		
DT	18-JUL-2000	(first entry)
DT		
DE	Mature human ztgfbeta-9 variant protein.	
XX		
XX	Human transforming growth factor beta-9; ztgf beta-9;	
KW	Alzheimer's disease; neurodegenerative disease; Huntington's disease;	
KW	amyotrophic lateral sclerosis; ALS; Parkinson's disease;	
KW	peripheral neuropathy; demyelinating disease; multiple sclerosis;	
KW	antiviral; cytostatic.	
XX		
OS		Homo sapiens .
XX		
PN		WO200015798-A2.

PD 23-MAR-2000.
XX

Presnell SR, Taft DW, Foley KP;
XX 17-SEP-1988; 98US-0154817.
XX (ZYMO) ZYMOGENETICS INC.
PA PI

DR WPI; 2000-271436/23.
DD N.D.C.D.P. 2000-2752201

XX PT Polynucleotides encoding a novel transforming growth factor beta-9

PT XX antiproliferative agent

CC factor beta-9 protein, designated Ztgf beta-9. Human Ztgf beta-9 was CC isolated from an arrayed pituitary gland cDNA plasmid library by PCR CC screening. This can be used to treat a variety of neurodegenerative CC diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's CC disease, Huntington's disease, Parkinson's disease and peripheral CC neuropathies, or demyelinating diseases including multiple sclerosis CC and MS.

CC Ztgf beta-9 peptides have antiviral activity and may also be used to CC regulate the proliferation, differentiation and apoptosis of neurons CC and glial cells, lymphocytes, hematopoietic cells and stromal cells.

SQ Sequence 187 AA;

```

Query Match          100 0%; Score 729; DB 21; Length 187;
Best Local Similarity 100 0%; Pred. No. 1.4e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy   1 SCPAGGRPADRFRTPTNLRSVSPMAYRISVPDARYPRYLPDEAYCUCRGCLTGLEEDVY 60

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Best Local Similarity	100.0%	Pred. No.	1.2e-74;	Mismatches	0;	Indels	0;	Gaps	0;	
Matches	133;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
QY	1	SCPAGGRPADRRFPPPTNLSRSPWAIISYDARYPAPYLPEAYCLRGCLIGLFGEEDV	60	QY	1	SCPAGGRPADRRFPPPTNLSRSPWAIISYDARYPAPYLPEAYCLRGCLIGLFGEEDV	60			
Db	41	scpaggrpadrrfppptnlsrspwaiisydarypapylpeayclrgcliglfgeedv	100	Db	53	scpaggrpadrrfppptnlsrspwaiisydarypapylpeayclrgcliglfgeedv	112			
QY	61	RFRSAPAVMPVTWLRTTPACAGGRSVTPEAKVTPVGCTVPEKEKDADSINSSIDKOGA	120	QY	61	RFRSAPAVMPVTWLRTTPACAGGRSVTPEAKVTPVGCTVPEKEKDADSINSSIDKOGA	120			
Db	101	rfrsapavmpvtwlrttpacaggrsvtpeakytipvgctvpekdadsinsidkoga	160	Db	113	rfrsapavmpvtwlrttpacaggrsvtpeakytipvgctvpekdadsinsidkoga	172			
QY	121	KLLGPNDAPAGP	133	QY	121	KLLGPNDAPAGP	133			
Db	161	kllgpdapagp	173	Db	173	kllgpdapagp	185			
<hr/>										
RESULT	3			RESULT	4					
AYT0656		AAV70656 *standard; Protein; 185 AA.		AYT0655		AAV70655 standard; Protein; 186 AA.				
TD		AAV70656		ID		AAV70655				
XX				XX						
AC		AAV70656;		AC		AAV70655;				
XX				XX						
DT	18-JUL-2000	(first entry)		DT	18-JUL-2000	(first entry)				
XX				XX						
DE	Mature human transforming growth factor beta-9,	Ztgfbeta-9 protein-2.		DE	Mature human transforming growth factor beta-9,	Ztgfbeta-9,				
XX				XX						
XX	Human transforming growth factor beta-9; Ztgf beta-9;			XX	Human transforming growth factor beta-9; Ztgf beta-9;					
KW	Alzheimer's disease; neurodegenerative disease; Huntington's disease;			KW	Alzheimer's disease; neurodegenerative disease; Huntington's disease;					
KW	amyotrophic lateral sclerosis; ALS; Parkinson's disease;			KW	amyotrophic lateral sclerosis; ALS; Parkinson's disease;					
KW	peripheral neuropathy; demyelinating disease; multiple sclerosis;			KW	peripheral neuropathy; demyelinating disease; multiple sclerosis;					
KW	antiviral; cytostatic.			XX						
OS	Homo sapiens.			OS	Homo sapiens.					
XX				XX						
PN	WO200015798-A2.			PN	WO200015798-A2.					
XX				XX						
PD	23-MAR-2000.			PD	23-MAR-2000.					
XX				XX						
PF	17-SEP-1999;	99WO-US21677.		PF	17-SEP-1999;	99WO-US21677.				
XX				XX						
PR	17-SEP-1998;	98US-0154817.		PR	17-SEP-1998;	98US-0154817.				
XX				XX						
PA	(ZYMO) ZYMOGENETICS INC.			PA	(ZYMO) ZYMOGENETICS INC.					
XX				XX						
PI	Presnell SR, Taft DW, Foley KP;			PI	Presnell SR, Taft DW, Foley KP;					
XX				XX						
DR	WPI: 2000-271436/23.			DR	WPI: 2000-271436/23.					
XX				XX						
N-PSDB;	AAZ52195.			N-PSDB;	AAZ52195.					
PS	Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated Ztgf beta-9, useful as an antiviral and anti-proliferative agent -			PS	Polynucleotides encoding a novel transforming growth factor beta-9 polypeptide, designated Ztgf beta-9, useful as an antiviral and anti-proliferative agent -					
XX				XX						
PS	Claim 6; Page 85-86; 97pp; English.			PS	Claim 6; Page 84; 97pp; English.					
XX				XX						
CC	The present sequence is the mature human transforming growth factor beta-9, designated Ztgf beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 18 to and including amino acid 202 of Ztgf beta-9. Human Ztgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.			CC	The present sequence is the mature human transforming growth factor beta-9, designated Ztgf beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 17 to and including amino acid 202 of Ztgf beta-9. Human Ztgf beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.					
CC				CC						
CC	Sequence 185 AA;			CC	Sequence 186 AA;					
Query Match	100.0%	Score	729;	DB	21;	Length	186;			
Best Local Similarity	100.0%	Pred. No.	1.3e-74;							
Matches	133;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	

GenCore version 4.5
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protein - protein search, using sw model

run on: October 5, 2001, 15:19:50 ; Search time 21.13 Seconds
(without alignments)
381.590 Million cell updates/sec

title: US-09-320-713-4_COPY_28_160
ref. score: 7.79
sequence: 1 SCPGGRPADRRFRPTNIR.....SIDKQGAKLILGPNDAPAGP 133

scoring table: BLOSUM62
gapop 10.0 , Gapext 0.5

number of hits satisfying chosen parameters: 412676

minimum DB seq length: 0
maximum DB seq length: 2000000000

hit-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database :

```

1: /SIDS8/gcgdata/geneseq/geneseq/AAI1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseq/AAI1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/AAI1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseq/AAI1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseq/AAI1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseq/AAI1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseq/AAI1986.DAT:*
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	729	100.0	160	21	AAV53893		Partial amino acid
2	729	100.0	173	21	AAV53893		Mature human trans
3	729	100.0	185	21	AAV70656		Mature human trans
4	729	100.0	186	21	AAV70655		Mature human trans
5	729	100.0	187	21	AAV70654		Mature human trans
6	729	100.0	187	21	AAV70663		Mature human Ztgfb
7	729	100.0	202	21	AAB07595		A human interleuk
8	729	100.0	202	21	AAB07689		A human interleuk
9	729	100.0	202	21	AAV70653		Human transforming
10	729	100.0	209	21	AAV70662		Human transforming
11	613	84.1	151	21	AAB07594		A human interleuk

ALIGNMENT S

RESULT 1
 AAY33891
 ID AAY33891 standard; Protein: 160 AA.
 XX
 AC AAY33891;
 XX
 DT 13-MAR-2000 (first entry)
 DE Partial amino acid sequence of human interleukin-22.
 KW Human; interleukin-22; IL-22; IL-21; immune system disorder;
 KW immune cell chemotaxis; haematopoietic cell disorder;
 KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
 KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;
 KW inflammation; hyperproliferative disorder; tissue regeneration;
 KW embryonic stem cell differentiation; embryonic stem cell proliferation;
 KW haematopoietic lineage; allergic asthma.

SUMMARIES

S	Score	Query	Match	Length	DB	ID	Description	
							Amino acid	Amino acid
1	729	100_0	160	21	AY53891		Partial	amino acid
2	729	100_0	173	21	AY53893		Partial	amino acid
3	729	100_0	185	21	AYT0656		Mature	human trans
4	729	100_0	186	21	AYT0655		Mature	human trans
5	729	100_0	187	21	AYT0654		Mature	human trans
6	729	100_0	187	21	AYT0663		Mature	human ZtgF1
7	729	100_0	202	21	AABT595		A	human interleukin
8	729	100_0	202	21	AABT689		A	human interleukin
9	729	100_0	202	21	AYT0653		Human	transforming
10	729	100_0	209	21	AABT662		Human	transforming
11	613	84_1	151	21	AABT594		A	human interleukin

XX	Key	Location/Qualifiers
PH	Modified-site	26
FT		/note= "potential N-linked glycosylation site"
FT	Domain	57..64
FT		/note= "conserved domain I"
FT	Domain	72..77
FT		/note= "conserved domain II"
FT	Domain	99..105
FT		/note= "conserved domain III"
FT	Domain	121..128
FT		/note= "conserved domain IV"
FT	Modified-site	139
FT		/note= "potential N-linked glycosylation site"
XX		